

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:11 ; Search time 84.1064 Seconds
(without alignments)
1843.986 Million cell updates/sec

Title: US-09-389-782A-2
Perfect score: 2179
Sequence: 1 MNKWCCALLVLLDIEWT.....QKLFLEMIGNQVSKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2179	100.0	401	2 AAW38344	Aaw38344 Mouse ost
2	2179	100.0	401	4 AAB80898	Aab80898 Human ost
3	2179	100.0	401	4 AAY72916	Aay72916 Human ost
4	2179	100.0	401	4 AAB66975	Aab66975 Murine OP
5	2179	100.0	401	8 ADM28811	Adm28811 Mouse ost
6	2079	95.4	401	2 AAW38343	Aaw38343 Rat osteo
7	2079	95.4	401	4 AAB66974	Aab66974 Rat OPG.
8	2079	95.4	401	8 ADM28809	Adm28809 Rat osteo
9	2061	94.6	380	4 AAB66987	Aab66987 Human OPG
10	2061	94.6	380	8 ADM28826	Adm28826 Mouse ost
11	2050	94.1	380	8 ADM28861	Adm28861 Mouse ost
12	1900	87.2	401	2 AAY05742	Aay05742 Tumour ne
13	1900	87.2	401	2 AAW95030	Aaw95030 Tumour ne
14	1900	87.2	401	2 AAW83926	Aaw83926 Human FTH
15	1900	87.2	401	3 AAB18715	Aab18715 A human t
16	1900	87.2	401	4 AAB60570	Aab60570 Human TNF
17	1900	87.2	401	6 AAB36245	Aab36245 Human TRA
18	1900	87.2	401	6 AAO31135	Aao31135 Human TRA
19	1900	87.2	401	7 ADD01635	Add01635 Human ost
20	1900	87.2	401	7 ADF16158	Adf16158 Human alb
21	1900	87.2	401	7 ADF16153	Adf16153 Human alb
22	1900	87.2	401	7 ADF16151	Adf16151 Human alb
23	1900	87.2	401	7 ADF15231	Adf15231 Human alb
24	1900	87.2	401	7 ADF16152	Adf16152 Human alb
25	1900	87.2	401	7 ADF16154	Adf16154 Human alb

26	1900	87.2	401	7 ADF16155	Adf16155 Human alb
27	1900	87.2	401	7 ADF16156	Adf16156 Human alb
28	1900	87.2	401	7 ADF15230	Adf15230 Human alb
29	1900	87.2	401	7 ADF15244	Adf15244 Human alb
30	1900	87.2	401	7 ADF16157	Adf16157 Human alb
31	1900	87.2	401	8 ADK82154	Adk82154 Human TRA
32	1900	87.2	986	7 ADF15016	Adf15016 Human alb
33	1900	87.2	986	7 ADF15030	Adf15030 Human alb
34	1895	87.0	401	2 AAW99925	Aaw99925 Full leng
35	1895	87.0	401	2 AAW53239	Aaw53239 Human OCI
36	1895	87.0	401	3 AAY88622	Aay88622 Osteoclas
37	1895	87.0	401	6 ABP70997	Abp70997 Human ost
38	1895	87.0	401	7 ADD37427	Add37427 Human ost
39	1895	87.0	401	8 ADQ68056	Adq68056 Human ost
40	1892	86.8	401	2 AAW38345	Aaw38345 Human ost
41	1892	86.8	401	3 AAY43400	Aay43400 Osteoprot
42	1892	86.8	401	4 AAB66976	Aab66976 Human OPG
43	1892	86.8	401	5 ABG71823	Abg71823 Wild type
44	1892	86.8	401	6 ABP55109	Abp55109 Human ost
45	1892	86.8	401	6 AAE34363	Aae34363 Human ost

ALIGNMENTS

RESULT 1
AAW38344
ID AAW38344 standard; protein; 401 AA.

AC AAW38344;

DT 20-APR-1998 (first entry)

DE Mouse osteoprotegerin.

XX
XX
KW Osteoprotegerin; antibody; diagnosis; affinity purification;
KW recombinant production; transgenic animal; treatment; prevention;
KW antisense oligonucleotide; probe; detection; screening; mouse;
KW bone disease; osteoporosis; Paget's disease; hypercalcaemia;
KW hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
KW osteolytic metastasis; periodontal bone loss; bone necrosis; osteopaenia;
KW murine.

XX Mus sp.

EH Key Location/Qualifiers
FT CDS 90..1295
FT /tag=a
FT /product="osteoprotegerin"

FT DE19654610-A1.

PD 26-JUN-1997.

XX 20-DEC-1996; 96DE-01054610.

XX 22-DEC-1995; 95US-00577788.

PR 03-SEP-1996; 96US-00706945.

XX (AMGE-) AMGEN INC.

PA Boyle WJ, Lacey DL, Calzone FJ, Chang M;

XX WPI; 1997-334271/31.

DR N-PSDB; AAT96062.

XX Nucleic acid encoding osteoprotegerin - useful for treatment of diseases

PT involving excessive bone loss, e.g. osteoporosis.

XX Claim 23; Page 106-107; 182pp; German.

XX The present sequence is mouse osteoprotegerin (OPG). Anti-OPG antibodies

CC can be used in OPG diagnostic assays, and as affinity purification

CC materials. The OPG cDNA can be used to express recombinant OPG and to
 CC generate transgenic animals. It can also be used to regulate the level of
 CC OPG in mammals, specifically to increase OPG levels, however the level of
 CC antisense sequences is also contemplated. Fragments of the cDNA can be
 CC used as probes to detect OPG expressing cells and tissue, and to screen
 CC cDNA libraries for related sequences. OPG can be used to treat or prevent
 CC bone diseases, specifically excessive bone loss, e.g. osteoporosis,
 CC Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid
 CC arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss,
 CC bone necrosis and osteopaenia

XX Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.6e-174;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIETWTTQETLPPKYLHYDPETHQLLCKAPGYLKHQCTVRRKT 60
 DB 1 MNKWLCCALLVLLDIIETWTTQETLPPKYLHYDPETHQLLCKAPGYLKHQCTVRRKT 60

QY 61 LCVPCPDHSYDTSWHTSDVCVYCSVKELQSVKQECNRTNHRVCEBEGRYLEIEFCLK 120
 DB 61 LCVPCPDHSYDTSWHTSDVCVYCSVKELQSVKQECNRTNHRVCEBEGRYLEIEFCLK 120

QY 121 HRSCPPGSGVQAGTPERNVTCKCPDGFSGTSSKAPCIKHTNCSFGILLIQGNAT 180
 DB 121 HRSCPPGSGVQAGTPERNVTCKCPDGFSGTSSKAPCIKHTNCSFGILLIQGNAT 180

QY 181 HDNVCSGNREATQKCGIDVTLCEAFRRFAVPTKIIPNWLSVLDSPGTVKNAESVERI 240
 DB 181 HDNVCSGNREATQKCGIDVTLCEAFRRFAVPTKIIPNWLSVLDSPGTVKNAESVERI 240

QY 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKKIIQDIDLCESSVQRHGHNSLTTEQLLALME 300
 DB 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKKIIQDIDLCESSVQRHGHNSLTTEQLLALME 300

QY 301 SLPGKKISPEIERTRKTKSSSEQLLKLILWRIKNGQDITLKLWYALKHLKTSHPFKT 360
 DB 301 SLPGKKISPEIERTRKTKSSSEQLLKLILWRIKNGQDITLKLWYALKHLKTSHPFKT 360

QY 361 VTHSLRKTMRFHLSMTMRLLYQKLFLEMIGNOVQSVKISCL 401
 DB 361 VTHSLRKTMRFHLSMTMRLLYQKLFLEMIGNOVQSVKISCL 401

RESULT 2

AAB80898
 ID AAB80898 standard; protein; 401 AA.

XX AAB80898;

DT 31-MAY-2001 (first entry)

DE Human osteoprotegrin, OPG.

XX Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
 KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
 KW osteoclast formation inhibition; bone resorption inhibition.

XX Homo sapiens.

XX WO200117543-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-US022806.

XX 03-SEP-1999; 99US-00389545.

XX (AMGE-) AMGEN INC.

XX Dunstan CR;

XX WPI; 2001-265936/27.

DR Preventing or treating lytic bone diseases, particularly associated with
 PT cancer or metastasis, by administering an osteoprotegrin polypeptide.

XX Claim 5; Fig 2; 87pp; English.

CC The present invention relates to a method for the prevention or treatment
 CC of lytic bone disease or multiple myeloma. Also the method can be used
 CC for preventing metastasis of cancer to bone or osteosclerotic bone
 CC metastasis. The method comprises administering an OPG (osteoprotegrin)
 CC polypeptide or OPG fusion protein (see AAB80899-AAB80904). The present
 CC sequence is human OPG. OPG inhibits formation of osteoclasts (and thus
 CC bone resorption) by blocking differentiation from monocytes/macrophage
 CC precursors. The OPG polypeptide can be used in a method of preventing or
 CC treating lytic bone disease, for preventing metastasis of cancer to bone
 CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
 CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
 CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic
 CC bone metastasis. The OPG fusion polypeptides are used in the prevention
 CC or treatment of loss of bone mass, which occurs in conditions including
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
 CC congenital forms of osteoporosis (osteogenesis imperfecta,
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
 CC hyperthyroidism and renal function disorders; osteopaenia following
 CC surgery, induced by steroid administration, and associated with disorders
 CC of the small and large intestine and with chronic hepatic and renal
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
 CC are also used in the replacement of structurally sound bone with
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
 CC in adults and juveniles; hyperparathyroidism, in congenital bone
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone
 CC metastases

XX Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.6e-174;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIETWTTQETLPPKYLHYDPETHQLLCKAPGYLKHQCTVRRKT 60
 DB 1 MNKWLCCALLVLLDIIETWTTQETLPPKYLHYDPETHQLLCKAPGYLKHQCTVRRKT 60

QY 61 LCVPCPDHSYDTSWHTSDVCVYCSVKELQSVKQECNRTNHRVCEBEGRYLEIEFCLK 120
 DB 61 LCVPCPDHSYDTSWHTSDVCVYCSVKELQSVKQECNRTNHRVCEBEGRYLEIEFCLK 120

QY 121 HRSCPPGSGVQAGTPERNVTCKCPDGFSGTSSKAPCIKHTNCSFGILLIQGNAT 180
 DB 121 HRSCPPGSGVQAGTPERNVTCKCPDGFSGTSSKAPCIKHTNCSFGILLIQGNAT 180

QY 181 HDNVCSGNREATQKCGIDVTLCEAFRRFAVPTKIIPNWLSVLDSPGTVKNAESVERI 240
 DB 181 HDNVCSGNREATQKCGIDVTLCEAFRRFAVPTKIIPNWLSVLDSPGTVKNAESVERI 240

QY 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKKIIQDIDLCESSVQRHGHNSLTTEQLLALME 300
 DB 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKKIIQDIDLCESSVQRHGHNSLTTEQLLALME 300

QY 301 SLPGKKISPEIERTRKTKSSSEQLLKLILWRIKNGQDITLKLWYALKHLKTSHPFKT 360
 DB 301 SLPGKKISPEIERTRKTKSSSEQLLKLILWRIKNGQDITLKLWYALKHLKTSHPFKT 360

Db 301 SLPGKKISPEEIERTRKTKSSBQLKLLSLWRIKNGDQDTLKGMLYALKHLKTSHPKPT 360

QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 3

AA72916

ID AAY72916 standard; protein; 401 AA.

XX

AC AAY72916;

DT 13-JUN-2001 (first entry)

XX

DE Human osteoprotegerin (OPG).

XX

KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;

KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;

KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;

KW periodontal.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..21

FT /label= Signal_peptide

FT Protein 22..401

FT /label= Mature_osteoprotegerin

XX

PN WO200118203-A1.

PD 15-MAR-2001.

XX

PD 18-AUG-2000; 2000WO-US022797.

XX

XX 03-SEP-1999; 99US-00389782.

PR (AMGE-) AMGEN INC.

XX

PI Dunstan CR, Wooden SK, Mann MB;

XX

XX WPI; 2001-244572/25.

DR

XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused

PT by e.g. osteoporosis, Paget's disease and osteomyelitis.

XX

PS Claim 4; Fig 2; 119pp; English.

XX

CC The present sequence is human osteoprotegerin (OPG) protein. This

CC sequence is fused with the Fc region of human immunoglobulin G1 (IgG1) by

CC a linker sequence to form a fusion protein. OPG negatively regulates the

CC formation of osteoclasts in vitro and in vivo. It blocks the

CC differentiation of osteoclasts from monocyte or macrophage precursors and

CC the reabsorption of bone. The OPG-Fc fusion protein is administered for

CC the treatment of bone loss resulting from osteoporosis, Paget's disease,

CC osteomyelitis, hypercalcaemia, osteopenia associated with surgery or

CC steroid administration, osteonecrosis, bone loss due to rheumatoid

CC arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic

CC loosening

XX

SX Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 4; Length 401;

Best Local Similarity 100.0%; Pred. No. 2.6e-174;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIETWTQTLPKYLHYDPETGHQLLCKDKCAPGTLYLKQHCTVRRKT 60

Db 1 MNKWLCCALLVLDIIETWTQTLPKYLHYDPETGHQLLCKDKCAPGTLYLKQHCTVRRKT 60

QY 61 LCVPCPDHSYTDSWHTSDECVYCSVCKELQSVKQECNTHNRVCECEBGRYLEIEFCLK 120

Db 61 LCVPCPDHSYTDSWHTSDECVYCSVCKELQSVKQECNTHNRVCECEBGRYLEIEFCLK 120

QY 121 HRSCPPGGVQAGTPERNTVCKKCPDGFSGFSTSSKAPCIKHTNCSTFGLLLIQKNAT 180

Db 121 HRSCPPGGVQAGTPERNTVCKKCPDGFSGFSTSSKAPCIKHTNCSTFGLLLIQKNAT 180

QY 181 HDNVCSGNREATQKCGIDVTLCSEAFPRPAVTKIIPNWLVSVDLSLPTKNAESVERI 240

Db 181 HDNVCSGNREATQKCGIDVTLCSEAFPRPAVTKIIPNWLVSVDLSLPTKNAESVERI 240

QY 241 KRRHSSQEQTFOLLKWKHQRDQEMVKIIOIDILCESSVQRHLGHSNLTTEQLLALME 300

Db 241 KRRHSSQEQTFOLLKWKHQRDQEMVKIIOIDILCESSVQRHLGHSNLTTEQLLALME 300

QY 301 SLPGKKISPEEIERTRKTKSSBQLKLLSLWRIKNGDQDTLKGMLYALKHLKTSHPKPT 360

Db 301 SLPGKKISPEEIERTRKTKSSBQLKLLSLWRIKNGDQDTLKGMLYALKHLKTSHPKPT 360

QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 4

AAB66975

ID AAB66975 standard; protein; 401 AA.

XX

AC AAB66975;

DT 19-APR-2001 (first entry)

XX

DE Murine OPG.

XX

KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;

KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;

KW systemic lupus erythematosus; graft-versus-host disease; septic shock;

KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;

KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;

KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;

KW ischaemia; Parkinson's disease.

XX

OS Mus sp.

XX

PN WO200103719-A2.

XX

PD 18-JAN-2001.

XX

PF 07-JUL-2000; 2000WO-US018667.

XX

PR 09-JUL-1999; 99US-00350670.

PR 09-DEC-1999; 99US-00457647.

XX

PA (AMGE-) AMGEN INC.

XX

PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX

DR WPI; 2001-103031/11.

DR N-PSDB; AAF57837.

XX

PT Treating conditions leading to bone loss such as rheumatoid arthritis,

PT multiple sclerosis and asthma, comprises administering an osteoprotegerin

PT protein in conjunction with e.g. inhibitors of interleukin and tumor

PT necrosis factor alpha.

XX

PS Example 5; Fig 9; 316pp; English.

XX

CC The present invention relates to a method for treating conditions leading

CC to bone loss. The method comprises administering a purified and isolated

CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)

CC in conjunction with other substances such as tumour necrosis factor-alpha

CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE

CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet

activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock

Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.6e-174;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIETWTQETLPKYLHYDPETHQLLCDKAPGTYLKQHCTVRRKT 60
Db 1 MNKWLCCALLVLDIIETWTQETLPKYLHYDPETHQLLCDKAPGTYLKQHCTVRRKT 60

QY 61 LCVPCPDHSTYDSWHTSDCVYSPVCKELQSVKQECNTRNVCCEBGRYLEIEFCLK 120
Db 61 LCVPCPDHSTYDSWHTSDCVYSPVCKELQSVKQECNTRNVCCEBGRYLEIEFCLK 120

QY 121 HRSCPPGSGVQAGTPERNTVCKCPDPGFFSGTSSKAPCIKHTNGSTFGLLLIQGNAT 180
Db 121 HRSCPPGSGVQAGTPERNTVCKCPDPGFFSGTSSKAPCIKHTNGSTFGLLLIQGNAT 180

QY 181 HDNVCSGNRENTOKGIDVTLCEEAFFRAVPTKIIPNWLVDVSLPOTKNAESVERI 240
Db 181 HDNVCSGNRENTOKGIDVTLCEEAFFRAVPTKIIPNWLVDVSLPOTKNAESVERI 240

QY 241 KRHSSEQTFOLLKLWKHQNDRQENVKIIQIDLCSSVORHLGHSNLTTEQLALME 300
Db 241 KRHSSEQTFOLLKLWKHQNDRQENVKIIQIDLCSSVORHLGHSNLTTEQLALME 300

QY 301 SLPGKKISPEETERTKTKCSSEQLLKLWLRIKNGDQDTLKGLMYALKHLKTSHPFKT 360
Db 301 SLPGKKISPEETERTKTKCSSEQLLKLWLRIKNGDQDTLKGLMYALKHLKTSHPFKT 360

QY 361 VTHSLRKTRWFLHSFTMYRLYOKLFLEMTGNQVQSVKISCL 401
Db 361 VTHSLRKTRWFLHSFTMYRLYOKLFLEMTGNQVQSVKISCL 401

RESULT 5
ADM28811
ID ADM28811 standard; protein; 401 AA.

XX AC ADM28811;

DT 20-MAY-2004 (first entry)

XX Mouse osteoprotegerin, OPG.

XX Mouse; OPG; bone resorption; excessive bone loss; osteoporosis;
KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
KW steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;
KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
KW Riley-Day syndrome; immobilisation of extremity; tumour;
KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;
KW osteoprotegerin; transgenic.

OS Mus sp.

XX Location/Qualifiers

FT Key 1..21

FT Peptide /note= "Signal peptide"

FT Protein 22..401

FT /note= "Mature OPG"

FT Region 22..201
FT /note= "Claimed in claim 32"
FT Region 22..194
FT /note= "Claimed in claim 32"
FT Region 22..189
FT /note= "Claimed in claim 32"
FT Region 22..185
FT /note= "Claimed in claim 32"
FT Region 27..401
FT /note= "Claimed in claim 35"
FT Region 27..194
FT /note= "Claimed in claim 35"
FT Region 27..189
FT /note= "Claimed in claim 35"
FT Region 27..185
FT /note= "Claimed in claim 35"
FT Region 32..401
FT /note= "Claimed in claim 35"

US2003207827-A1.

PD 06-NOV-2003.

XX 24-SEP-1999; 99US-00405032.

XX 22-DEC-1995; 95US-005777788.

PR 03-SEP-1996; 96US-00706945.

PR 20-DEC-1996; 96US-00771777.

PR 12-AUG-1998; 98US-00132985.

XX (BOYL/) BOYLE W J.

PA (LACE/) LACEY D L.

PA (CALZ/) CALZONE F J.

XX (CHAN/) CHANG M.

PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;

XX WPI; 2004-041572/04.

DR N-PSDB; ADM28810.

XX Novel osteoprotegerin useful for treating conditions resulting in bone loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone loss caused by rheumatoid arthritis or osteomyelitis.

Claim 23; SEQ ID NO 123; 141pp; English.

The invention relates to a purified and isolated polypeptide having osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or having amino terminus at residue 22, and 1-216 amino acids are deleted from carboxy terminus of human OPG polypeptide. Also included are an isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression vector comprising OPG NA, a host cell transformed or transfected with the polypeptide comprising an amino acid sequence of at least about 164 amino acids comprising four cysteine-rich domains characteristic of the cysteine rich domains of tumour necrosis factor receptor extracellular regions (and an activity of increasing bone density), an antibody (Ab) or its fragment which specifically binds to OPG, a composition comprising OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant) and an osteoprotegerin multimer consisting of osteoprotegerin monomers. Ab is useful for detecting the presence of OPG in a biological sample which involves incubating the sample with Ab under conditions that allow binding of Ab to OPG and detecting the bound Ab. OPG is useful for assessing the ability of a candidate substance to bind to OPG. OPG NA is useful for regulating the levels of OPG in an animal (human). The nucleic acid promotes an increasing in tissue level of OPG. OPG is useful for treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to osteomyelitis, osteolytic metastasis, and periodontal bone loss. The method further involves administering a substance chosen from bone morphogenic protein BMP-1 through BMP-12, TGF-beta family members, Il-1 inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,

CC parathyroid hormone related protein and their analogues, B series; of
 CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
 CC useful for treating osteoporosis such as primary osteoporosis, endocrine
 CC osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),
 CC hereditary and congenital forms of osteoporosis (osteogenesis imperfecta
 CC, homocystinuria, Menke's syndrome, and Riley-day syndrome) and
 CC osteoporosis due to immobilisation of extremities, hypercalcaemia
 CC resulting from solid tumours and haematologic malignancies (multiple
 CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
 CC hypercalcaemia associated with hyperthyroidism and renal function.
 CC disorders, osteopaenia following surgery and osteonecrosis or bone cell
 CC death. The present sequences is an OPG protein (or fragment).
 XX
 SQ Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 8; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.6e-174;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNKWLCCALLVLDIIIEWTTQETLPKYLHYDPETHGQLLCKAPGTYLKQHCCTVRRKT 60
 DB 1 MNKWLCCALLVLDIIIEWTTQETLPKYLHYDPETHGQLLCKAPGTYLKQHCCTVRRKT 60
 QY 61 LCVPCPDHSYTDSWHTSDCVYCSVPCKELQSVKQECNTHNRVCEBGRYLEIFCLK 120
 DB 61 LCVPCPDHSYTDSWHTSDCVYCSVPCKELQSVKQECNTHNRVCEBGRYLEIFCLK 120
 QY 121 HRSCPPGSGVQAGTPERNTVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
 DB 121 HRSCPPGSGVQAGTPERNTVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
 QY 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLVSLPGTKVNAESVERI 240
 DB 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLVSLPGTKVNAESVERI 240
 QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300
 DB 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300
 QY 301 SLPGKKISPEEIERTRKTKCSSEQLLKLWLRIKNGDQDTLKLGLMYALKHLKTSHPFKT 360
 DB 301 SLPGKKISPEEIERTRKTKCSSEQLLKLWLRIKNGDQDTLKLGLMYALKHLKTSHPFKT 360
 QY 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVQSVKISCL 401
 DB 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVQSVKISCL 401

RESULT 6
 AAW38343
 ID AAW38343 standard; protein; 401 AA.

XX AAW38343;
 AC AAW38343;
 XX
 DT 20-APR-1998 (first entry)
 DE Rat osteoprotegerin.
 XX
 KW Rat; osteoprotegerin; antibody; diagnosis; affinity purification;
 KW recombinant production; transgenic animal; treatment; prevention;
 KW antisense oligonucleotide; probe; detection; screening; bone disease;
 KW osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism;
 KW rheumatoid arthritis; osteomyelitis; osteolytic metastasis;
 KW periodontal bone loss; bone necrosis; osteopaenia.

OS Rattus sp.
 XX
 PN DE19654610-A1.
 XX
 PD 26-JUN-1997.
 XX
 PF 20-DEC-1996; 96DE-01054610.
 XX

PR 22-DEC-1995; 95US-00577788.
 PR 03-SEP-1996; 96US-00706945.
 XX (AMGE-) AMGEN INC.
 PA Boyle WJ, Lacey DL, Calzone FJ, Chang M;
 XX WPI; 1997-334271/31.
 DR N-PSDB; AAT96061.
 XX
 PT Nucleic acid encoding osteoprotegerin - useful for treatment of diseases
 XX involving excessive bone loss, e.g. osteoporosis.
 PS Claim 23; Page 102-104; 182pp; German.
 XX
 CC The present sequence is rat osteoprotegerin (OPG). Anti-OPG antibodies
 CC can be used in OPG diagnostic assays, and as affinity purification
 CC materials. The OPG cDNA can be used to express recombinant OPG and to
 CC generate transgenic animals. It can also be used to regulate the level of
 CC OPG in mammals, specifically to increase OPG levels, however the level of
 CC antisense sequences is also contemplated. Fragments of the cDNA can be
 CC used as probes to detect OPG expressing cells and tissue, and to screen
 CC cDNA libraries for related sequences. OPG can be used to treat or prevent
 CC bone diseases, specifically excessive bone loss, e.g. osteoporosis,
 CC Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid
 CC arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss,
 CC bone necrosis and osteopaenia
 XX
 SQ Sequence 401 AA;

Query Match 95.4%; Score 2079; DB 2; Length 401;
 Best Local Similarity 94.5%; Pred. No. 6.5e-166;
 Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MNKWLCCALLVLDIIIEWTTQETLPKYLHYDPETHGQLLCKAPGTYLKQHCCTVRRKT 60
 DB 1 MNKWLCCALLVLDIIIEWTTQETLPKYLHYDPETHGQLLCKAPGTYLKQHCCTVRRKT 60
 QY 61 LCVPCPDHSYTDSWHTSDCVYCSVPCKELQSVKQECNTHNRVCEBGRYLEIFCLK 120
 DB 61 LCVPCPDHSYTDSWHTSDCVYCSVPCKELQSVKQECNTHNRVCEBGRYLEIFCLK 120
 QY 121 HRSCPPGSGVQAGTPERNTVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
 DB 121 HRSCPPGSGVQAGTPERNTVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
 QY 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLVSLPGTKVNAESVERI 240
 DB 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLVSLPGTKVNAESVERI 240
 QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300
 DB 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300
 QY 301 SLPGKKISPEEIERTRKTKCSSEQLLKLWLRIKNGDQDTLKLGLMYALKHLKTSHPFKT 360
 DB 301 SLPGKKISPEEIERTRKTKCPSEQLLKLWLRIKNGDQDTLKLGLMYALKHLKTSHPFKT 360
 QY 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVQSVKISCL 401
 DB 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVQSVKISCL 401

RESULT 7
 AAB66974
 ID AAB66974 standard; protein; 401 AA.

XX AAB66974;
 AC AAB66974;
 XX
 DT 19-APR-2001 (first entry)
 XX
 DE Rat OPG.
 XX

Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graft-versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain; coronary condition; myocardial infarction; cancer; diabetes; psoriasis; endometriosis; fever; glomerulonephritis; inflammatory bowel disease; ischaemia; Parkinson's disease.

Rattus sp.

W0200103719-A2.

18-JAN-2001.

07-JUL-2000; 2000WO-US018667.

09-JUL-1999; 99US-00350670.

09-DEC-1999; 99US-00457647.

(AMGE-) AMGEN INC.

Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

WPI; 2001-103031/11.

N-PSDB; AAF57836.

Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an osteoprotegerin protein in conjunction with e.g. inhibitors of interleukin and tumor necrosis factor alpha.

Disclosure; Fig 2; 316pp; English.

The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAFS7836-AAFS7838 and AAB66974-AAB66976) in conjunction with other substances such as tumour necrosis factor-alpha (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock

Sequence 401 AA;

Query Match 95.4%; Score 2079; DB 4; Length 401;
Best Local Similarity 94.5%; Pred. No. 6.5e-166;
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

1 MNKWLCCALLVLLDIIEWTQTTPPKYLHYDPETHQOLLDCKCAPGYLKHQCTVRRKT 60
1 MNKWLCCALLVLLDIIEWTQTTPPKYLHYDPETHQOLLDCKCAPGYLKHQCTVRRKT 60
61 LCVPCPDHSYTDSDWHTSDBCVYCSVCKELOSVKQCNRTNHRVCEEGRYLEPCLK 120
61 LCVPCPDYSYTDSDWHTSDBCVYCSVCKELOSVKQCNRTNHRVCEEGRYLEPCLK 120
121 HRSCEPFGSGVQAGTPERTNTVCKPCDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
121 HRSCEPGLGLVLAQTPERTNTVCKPCDGFSGTSSKAPCKHTNCSSGLGLLIQKGNAT 180
181 HDNVCSGNREATOKGIDVTLCCEAFPPFAVPTKIIIPNWSLVDSLPCTKNAESVERI 240
181 HDNVCSGNREATQNGIDVTLCCEAFPPFAVPTKIIIPNWSLVDSLPCTKNAESVERI 240
241 KRRHSSQRTQFLLKLWKHQRNDQEMVKIIQDIDLCESSVQRHGHNSLNTTEQLLME 300

Db 241 KRRHSSQRTQFLLKLWKHQRNDQEMVKIIQDIDLCESSVQRHGHNSLNTTEQLLME 300
QY 301 SLPGKKISPEIERTRTKTCKSEQLLKLLSLRWIRKNGDQDTLKGMLYALKHLKTSHPFKT 360
Db 301 SLPGKKISPEIERTRTKTCKSEQLLKLLSLRWIRKNGDQDTLKGMLYALKHLKTSHPFKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYOKLPLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYOKLPLEMIGNOVQSVKISCL 401

RESULT 8

ADM28809

ID ADM28809 standard; protein; 401 AA.

XX ADM28809;

XX 20-MAY-2004 (first entry)

XX Rat osteoprotegerin, OPG.

Rat; OPG; bone resorption; excessive bone loss; osteoporosis; Paget's disease of bone; hypercalcaemia; hyperparathyroidism; steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis; osteolytic metastasis; periodontal bone loss; Cushing's syndrome; acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome; Riley-day syndrome; immobilisation of extremity; tumour; haematologic malignancy; multiple myeloma; lymphoma; leukaemia; renal function disorder; osteopaenia; osteonecrosis; bone cell death; osteoprotegerin; transgenic.

XX Rattus sp.

Key	Location/Qualifiers
Peptide	1..21
Protein	/note= "Signal peptide"
Region	22..401
Region	/note= "Mature OPG"
Region	22..201
Region	/note= "Claimed in claim 32"
Region	22..194
Region	/note= "Claimed in claim 32"
Region	22..189
Region	/note= "Claimed in claim 32"
Region	22..185
Region	/note= "Claimed in claim 32"
Region	27..401
Region	/note= "Claimed in claim 35"
Region	27..194
Region	/note= "Claimed in claim 35"
Region	27..189
Region	/note= "Claimed in claim 35"
Region	27..185
Region	/note= "Claimed in claim 35"
Region	32..401
Region	/note= "Claimed in claim 35"

US2003207827-A1.

06-NOV-2003.

24-SEP-1999; 99US-00405032.

22-DEC-1995; 95US-00577788.

03-SEP-1996; 96US-00706945.

20-DEC-1996; 96US-00771777.

12-AUG-1998; 98US-00132985.

(BOYL/) BOYLE W J.

(LACE/) LACEY D L.

(CALZ/) CALZONE F J.

(CHAN/) CHANG M.

XX PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;
 XX WPI; 2004-041572/04.
 DR N-PSDB; ADM28808.
 XX PT Novel osteoprotegerin useful for treating conditions resulting in bone
 PT loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone
 PT loss caused by rheumatoid arthritis or osteomyelitis.
 XX Claim 23; SEQ ID NO 121; 141pp; English.
 XX The invention relates to a purified and isolated polypeptide having
 CC osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or
 CC having amino terminus at residue 22, and 1-216 amino acids are deleted
 CC from carboxy terminus of human OPG polypeptide. Also included are an
 CC isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression
 CC vector comprising OPG NA, a host cell transformed or transfected with the
 CC vector, a transgenic mammal comprising the cell, producing OPG, a
 CC polypeptide comprising an amino acid sequence of at least about 164 amino
 CC acids comprising four cysteine-rich domains characteristic of the
 CC cysteine rich domains of tumour necrosis factor receptor extracellular
 CC regions (and an activity of increasing bone density), an antibody (Ab) or
 CC its fragment which specifically binds to OPG, a composition comprising
 CC OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant)
 CC and an osteoprotegerin multimer consisting of osteoprotegerin monomers.
 CC Ab is useful for detecting the presence of OPG in a biological sample
 CC which involves incubating the sample with Ab under conditions that allow
 CC binding of Ab to OPG and detecting the bound Ab. OPG is useful for
 CC assessing the ability of a candidate substance to bind to OPG. OPG NA is
 CC useful for regulating the levels of OPG in an animal (human). The nucleic
 CC acid promotes an increasing in tissue level of OPG. OPG is useful for
 CC treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's
 CC disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced
 CC osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to
 CC osteomyelitis, osteolytic metastasis, and periodontal bone loss. The
 CC method further involves administering a substance chosen from bone
 CC morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1
 CC inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,
 CC parathyroid hormone related protein and their analogues, E series of
 CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
 CC useful for treating osteoporosis such as primary osteoporosis, endocrine
 CC osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),
 CC hereditary and congenital forms of osteoporosis (osteogenesis imperfecta
 CC, homocystinuria, Menke's syndrome, and Riley-day syndrome) and
 CC osteoporosis due to immobilisation of extremities, hypercalcaemia
 CC resulting from solid tumours and haematologic malignancies (multiple
 CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
 CC hypercalcaemia associated with hyperthyroidism and renal function
 CC disorders, osteopaenia following surgery and osteonecrosis or bone cell
 CC death. The present sequences is an OPG protein (or fragment).
 XX SQ Sequence 401 AA;

Query Match 95.4%; Score 2079; DB 8; Length 401;
 Best Local Similarity 94.5%; Pred. No. 6.5e-166;
 Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIETWTQETLPKYLHYDPTGHLCDKCAPCTYLLKHCTVRRKT 60
 DB 1 MNKWLCCALLVLDIIETWTQETFPFKYLHYDPTGHLCDKCAPCTYLLKHCTVRRKT 60
 QY 61 LCVPCPDHSTYDSWHTSDCEVYSPVKELQSVKQECNTRHNRCVCEGRYLEIFCLK 120
 DB 61 LCVPCPDYSYTDWHTSDCEVYSPVKELQTVKQECNTRHNRCVCEGRYLEIFCLK 120
 QY 121 HRCSPGSGVQAGTPTERNVTCKPDGPFSGTSSKAPCIKNTNSTFGILLIQKNAT 180
 DB 121 HRCSPGGLVQAGTPTERNVTCKPDGPFSGTSSKAPCKRHTNCSLLGILLIQKNAT 180
 QY 181 HDNVCSGNREATCKGIDVTLCSEAFRFAVPTKIIIPNVLVDLSIPGCKVNAESVERI 240
 DB 181 HDNVCSGNREATCKGIDVTLCSEAFRFAVPTKIIIPNVLVDLSIPGCKVNAESVERI 240

QY 241 KRRHSSQEQTFQLLKLWKQHNDRDQENVVKIIQIDICLCESSVQRHLGHSNLTTFQLALME 300
 DB 241 KRRHSSQEQTFQLLKLWKQHNDRDQENVVKIIQIDICLCESSVQRHLGHSNLTTFQLALME 300
 QY 301 SLPGKKISPEETERTKTKCSFQLKLJSLWRIKNGDDDTLKLGMVYALKHLKLTSHPPKT 360
 DB 301 SLPGKKISPEETERTKTKCPSEQLKLJSLWRIKNGDDDTLKLGMVYALKHLKLTSHPPKT 360
 QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
 DB 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 9
 AAB66987
 ID AAB66987 standard; protein; 380 AA.
 XX AAB66987;
 AC AAB66987;
 XX 19-APR-2001 (first entry)
 DT Human OPG cysteine-rich domain.
 XX Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
 KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
 KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
 KW ischaemia; Parkinson's disease.
 XX Homo sapiens.
 OS WC200103719-A2.
 PN 18-JAN-2001.
 PD 07-JUL-2000; 2000WO-US018667.
 XX 09-JUL-1999; 99US-00350670.
 PR 09-DEC-1999; 99US-00457647.
 XX (AMGE-) AMGEN INC.
 PA Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
 WPI; 2001-103031/11.
 XX Treating conditions leading to bone loss such as rheumatoid arthritis,
 PT multiple sclerosis and asthma, comprises administering an osteoprotegerin
 PT protein in conjunction with e.g. inhibitors of interleukin and tumor
 PT necrosis factor alpha.
 XX Disclosure; Fig 12; 316pp; English.
 PS The present invention relates to a method for treating conditions leading
 CC to bone loss. The method comprises administering a purified and isolated
 CC osteoprotegerin (OPG) protein (AA657836-APF57838 and AAB66974-AAB66976)
 CC in conjunction with other substances such as tumour necrosis factor-alpha
 CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
 CC activating factor (PAF) antagonists. The method is useful for treating
 CC conditions leading to bone loss such as rheumatoid arthritis, multiple
 CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
 CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
 CC graft-versus-host disease (GVHD). Other diseases that can be treated
 CC include acute pancreatitis, Alzheimer's disease, anorexia,
 CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
 CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
 CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
 CC psoriasis and septic shock
 XX

Db 241 RDQEMVKKIIQDIDLCSSVQRHGHNSLTTEQLLALMESLPGRKISPEIERTRKTKCS 300
 QY 322 SEQLLKLSSLRIRKNGDQDTLKGIMVALKHLKTSHPFKTVTHSLRKTRMRLHSTMYRLY 381
 Db 301 SEQLLKLSSLRIRKNGDQDTLKGIMVALKHLKTSHPFKTVTHSLRKTRMRLHSTMYRLY 360
 QY 382 QKLFLEMIGNQVQSVKISCL 401
 Db 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 11
 ADM28861
 ID ADM28861 standard; protein; 380 AA.
 XX
 AC ADM28861;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Mouse osteoprotegerin cysteine-rich domains 1-4 plus C-terminus #2.
 XX
 KW Mouse; OPG; bone resorption; excessive bone loss; osteoporosis;
 KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
 KW steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;
 KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
 KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
 KW Riley-day syndrome; immobilisation of extremity; tumour;
 KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
 KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;
 KW osteoprotegerin; transgenic.
 XX
 OS Mus sp.
 XX
 XX US2003027827-A1.
 XX
 PD 06-NOV-2003.
 XX
 XX 24-SEP-1999; 99US-00405032.
 XX
 PR 22-DEC-1995; 95US-00577788.
 PR 03-SEP-1996; 96US-00706945.
 PR 20-DEC-1996; 96US-00717777.
 PR 12-AUG-1998; 98US-00132985.
 XX
 PA (BOYL/) BOYLE W J.
 PA (LACE/) LACEY D L.
 PA (CALZ/) CALZONE F J.
 PA (CHAN/) CHANG M.
 XX
 PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;
 XX WPI; 2004-041572/04.
 DR
 XX Novel osteoprotegerin useful for treating conditions resulting in bone
 PT loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone
 PT loss caused by rheumatoid arthritis or osteomyelitis.
 XX
 PS Example 6; Fig 12; 141pp; English.
 XX
 CC The invention relates to a purified and isolated polypeptide having
 CC osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or
 CC having amino terminus at residue 22, and 1-216 amino acids are deleted
 CC from carboxy terminus of human OPG polypeptide. Also included are an
 CC isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression
 CC vector comprising OPG NA, a host cell transformed or transfected with the
 CC polypeptide comprising an amino acid sequence of the cell, producing OPG, a
 CC acids comprising four cysteine-rich domains characteristic of the
 CC cysteine rich domains of tumour necrosis factor receptor extracellular
 CC regions (and an activity of increasing bone density), an antibody (Ab) or
 CC its fragment which specifically binds to OPG, a composition comprising
 CC OPG (in a carrier, adjuvant, stabiliser, and/or anti-oxidant)

CC and an osteoprotegerin multimer consisting of osteoprotegerin monomers.
 CC Ab is useful for detecting the presence of OPG in a biological sample
 CC which involves incubating the sample with Ab under conditions that allow
 CC binding of ab to OPG and detecting the bound Ab. OPG is useful for
 CC assessing the ability of a candidate substance to bind to OPG. OPG NA is
 CC useful for regulating the levels of OPG in an animal (human). The nucleic
 CC acid promotes an increasing in tissue level of OPG. OPG is useful for
 CC treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's
 CC disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced
 CC osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to
 CC osteomyelitis, osteolytic metastasis, and periodontal bone loss. The
 CC method further involves administering a substance chosen from bone
 CC morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1
 CC inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,
 CC parathyroid hormone related protein and their analogues, E series of
 CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
 CC useful for treating osteoporosis such as primary osteoporosis, endocrine
 CC osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),
 CC hereditary and congenital forms of osteoporosis (osteogenesis imperfecta
 CC , homocystinuria, Menke's syndrome, and Riley-day syndrome) and
 CC osteoporosis due to immobilisation of extremities, hypercalcaemia
 CC resulting from solid tumours and haematologic malignancies (multiple
 CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
 CC hypercalcaemia associated with hyperthyroidism and renal function
 CC disorders, osteopaenia following surgery and osteonecrosis or bone cell
 CC death. The present sequences is an OPG protein (or fragment).
 XX
 SQ Sequence 380 AA;
 Query Match 94.1%; Score 2050; DB 8; Length 380;
 Best Local Similarity 99.2%; Pred. No. 1.7e-163;
 Matches 377; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 22 ETLPKYLHYDPTGHQLLCKAPGYLKHQCTVRRKTLVCPDHSYTDSWHTSDECV 81
 Db 1 ETLPKYLHYDPTGHQLLCKAPGYLKHQCTVRRKTLVCPDHSYTDSWHTSDECV 60
 QY 82 YCSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLKHRSPPGSGVQAGTPERTV 141
 Db 61 YCSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLKHRSPPGSGVQAGTPERTV 120
 QY 142 CKKCPDGFSGTSSKAPCICKHTNCSTFGLLLOKGNATHDNYVCSGNREATQCGIDVTL 201
 Db 121 CKKCPDGFSGTSSKAPCICKHTNCSTFGLLLOKGNATHDNYVCSGNREATQCGIDVTL 180
 QY 202 CEAFPRFAVPTKIIIPNLSVLVDSLPGTKVNAESVERIKRHSSEQOTFQLLKLWKHQ 261
 Db 181 CEAFPRFAVPTKIIIPNLSVLVDSLPGTKVNAESVERIKRHSSEQOTFQLLKLWKHQ 240
 QY 262 RDQEMVKKIIQDIDLCSSVQRHGHNSLTTEQLLALMESLPGRKISPEIERTRKTKCS 321
 Db 241 RDQEMVKKIIQDIDLCSSVQRHGHNSLTTEQLLALMESLPGRKISPEIERTRKTKCS 300
 QY 322 SEQLLKLSSLRIRKNGDQDTLKGIMVALKHLKTSHPFKTVTHSLRKTRMRLHSTMYRLY 381
 Db 301 SEQLLKLSSLRIRKNGDQDTLKGIMVALKHLKTSHPFKTVTHSLRKTRMRLHSTMYRLY 360
 QY 382 QKLFLEMIGNQVQSVKISCL 401
 Db 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 12
 AAY05742
 ID AAY05742 standard; protein; 401 AA.
 XX
 AC AAY05742;
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE Tumour necrosis factor receptor TR1.
 XX Tumour necrosis factor receptor; TR1; osteoprotegerin; agonist;
 KW

antagonist; screening; human; cancer; AIDS; Alzheimer's disease; inflammation; arthritis; septicemia; autoimmune disease; psoriasis; inflammatory bowel disease; transplant rejection; graft versus host disease; infection; stroke; ischaemia; acute respiratory disease syndrome; restenosis; brain injury; bone disease; atherosclerosis; therapy.

Homo sapiens.

BP911633-A1.

28-APR-1999.

02-OCT-1998; 98EP-00203332.

08-OCT-1997; 97US-0061334P.

(SMIK) SMITHKLINE BEECHAM CORP.

McDonnell PC, Young PR, Zou J;

WPI; 1999-246560/21.

Identifying agonists and antagonists of tumor necrosis factor related receptors TR1, TR3 and TR5, and of ligand TL3, useful for treatment of cancer, AIDS, Alzheimer's disease, bone disease etc.

Disclosure; Page 10-12; 23pp; English.

The present sequence represents tumour necrosis factor receptor (TNFR) TR1, also known as osteoprotegerin. The invention relates to TNFR related polypeptides TR1, TR3 and TR5 (see AAY05742-44) and their ligand TL3 (see AAY05745). TR1, TR3, TR5 and TL3 are used in claimed methods of identifying agonists and antagonists, i.e. compounds that bind to the receptors or ligand, and which activate (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or TL3. A screening kit for identifying agonists, antagonists, ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or TL3 polypeptides is provided. The agonists and antagonists are useful for treatment of chronic and acute inflammation, arthritis, septicemia, autoimmune disease e.g. inflammatory bowel disease, psoriasis, transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders), atherosclerosis and Alzheimer's disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3

Sequence 401 AA;

Query Match 87.2%; Score 1900; DB 2; Length 401;
Best Local Similarity 85.8%; Pred. No. 7.2e-151;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLDI-IEWTQETLPPKYLHYDPTGQHLCDKCAPGYLKHQCTVRRK 59
DB 1 MNKLLCCA-LVFLDISIKWTQETFPKYLHYDETSQHLCDKCPGYLKHQCTAKWK 59

QY 60 TLVCPCPDHSTYDTSMTSDECVYSPCKELQSVQECNRNTRNVCEEGRYLBIFFCL 119
DB 60 TVCAPCPDHYTDSMTSDECLYSPCKELQSVQECNRNTRNVCEEGRYLBIFFCL 119

QY 120 KHRSCPPGSGVQAGTPERTNCKPCDGFSGETSSKAPCIKHTNCSTFGLLLTQKNA 179
DB 120 KHRSCPPGSGVQAGTPERTNCKPCDGFSGETSSKAPCRKHTNCSTFGLLLTQKNA 179

QY 180 THDNVCSGNREATKGGIDVTLCCEAFFFAFVPTKIIIPNWLVSVDLPGTKVNAESVER 239
DB 180 THDNICSGNSESTQKGGIDVTLCCEAFFFAFVPTKFTFNWLSVLDNLPGTKVNAESVER 239

QY 240 IKRHSQEQBTOLLKWLKHQRDQEMVKIIQDIDLCESSVQRHGLNSLTTEQLLALM 299
DB 240 IKRHSQEQBTOLLKWLKHQRDQEMVKIIQDIDLCESSVQRHGLNSLTTEQLSILM 299

QY 300 ESLPGKKISPEIERTRKTKCSQELLKLLSLWRINKGDDTLKGLMVALKHLKTSHPFK 359

DB 300 ESLPGKKVGAEDIENTKACKPSDQILKLLSLWRINKGDDTLKGLMHALKHSKYHFK 359
QY 360 TVTHSLRKTMRPLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
DB 360 TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

RESULT 13
AAW95030
ID AAW95030 standard; protein; 401 AA.
XX
AC AAW95030;
XX
DT 13-MAY-1999 (first entry)
XX
DE Tumour necrosis factor receptor (TNF-R) related polypeptide TR1.
XX
KW Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL4; arthritis; inflammation; septicemia; autoimmune disease; transplant rejection; graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS; acute respiratory disease syndrome; restenosis; bone disease; cancer; atherosclerosis; Alzheimer's disease.
XX
OS Unidentified.
XX
PN EP897114-A2.
XX
PD 17-FEB-1999.
XX
PF 04-JUN-1998; 98EP-00304424.
XX
PR 13-AUG-1997; 97US-0055513P.
PR 26-AUG-1997; 97US-0056980P.
PR 29-AUG-1997; 97US-0057550P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PI Bringham-Burke MR, Young PR;
XX WPI; 1999-134308/12.
XX
PT Identifying agonists and antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (LR1, LR2, LR2 and LR4) - useful for treating stroke, Alzheimer's disease and AIDS.
XX
PS Disclosure; Page 11-12; 18pp; English.
XX
CC The invention relates to identifying agonists or antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2 and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2 or TL4 with a candidate compound in the presence of TR1 or TR2; and (b) assessing the ability of the candidate compound to compete with TR1 or TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful for treating diseases caused by imbalance of TL or TR polypeptide levels, which cause: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, transplant rejection, graft vs. host disease, infection, stroke, ischemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and Alzheimer's disease. The present sequence represents a TNF-R related polypeptide TR1

Sequence 401 AA;

Query Match 87.2%; Score 1900; DB 2; Length 401;
Best Local Similarity 85.8%; Pred. No. 7.2e-151;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLDI-IEWTQETLPPKYLHYDPTGQHLCDKCAPGYLKHQCTVRRK 59
DB 1 MNKLLCCA-LVFLDISIKWTQETFPKYLHYDETSQHLCDKCPGYLKHQCTAKWK 59

QY 60 TLVCPDHSYTDSTWHTSDVCYVSPVCKELQSVKQECNRTNHRVCECEGRYLEIEFCL 119
Db 60 TVCAPCPDHYTDSWHTSDVCLYVSPVCKELQVYKQECNRTNHRVCECEGRYLEIEFCL 119
QY 120 KHRSCPPGSGVQAGTPPERNTVCKCPDGFSSGETSSKAPCIKHNTCMSTFGLLLIQKNA 179
Db 120 KHRSCPPGSGVQAGTPPERNTVCKCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKNA 179
QY 180 THDNVCSGNREATQCGIDVTLCCEAFPRFAVPTKII PNWLSVLDLSLPGTKVNAESVER 239
Db 180 THDNICSGNSESTQCGIDVTLCCEAFPRFAVPTKFTPNWLSVLDNLPCTKVNAESVER 239
QY 240 IKRHSSQEQTFQLLKWKHQRNDQEWVKIIQDIDLCESSVQRHGHNLTEQLLALM 299
Db 240 IKRHSSQEQTFQLLKWKHQRNDQVVKIIQDIDLCESSVQRHGHNLTEQLLALM 299
QY 300 ESIPGKKISPEIERTRTKCKSEQLLKLKSLWRIKNGQDQTLKGLMYALKHLKTSHPFK 359
Db 300 ESIPGKKVGAEDIEKTIKACKPSDQILKLSLWRIKNGQDQTLKGLMHALKHKSHTYHPFK 359
QY 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
Db 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 14

AAW83926

ID AAW83926 standard; protein; 401 AA.

XX AC AAW83926;

XX XX

XX DT 01-MAR-1999 (first entry)

XX DE Human FTHMA-070 protein.

XX KW FTHMA-070; human; neurological disorder; therapy; diagnosis.

XX OS Homo sapiens.

XX XX

XX FH Key

XX FT Peptide

XX FT Protein

XX FT

XX PN WO9848051-A2.

XX PD 29-OCT-1998.

XX PF 17-APR-1998; 98WO-US007714.

XX PR 18-APR-1997; 97US-0044746P.

XX PR 10-OCT-1997; 97US-0062017P.

XX XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX PA McCarthy SA, Holtzman D;

XX PI WPI; 1999-024021/02.

XX DR N-PSDB; AAV69277.

XX XX

XX PT New isolated human FTHMA-070 and T85 proteins - used to develop products

XX PT for the diagnosis and therapy of disorders involving cellular processes,

XX PT e.g. neuronal development.

XX PS Claim 8; Fig 1; 127pp; English.

XX CC

XX CC This is the amino acid sequence of human FTHMA-070, a novel protein

XX CC having homology to tumour necrosis factor receptor. The sequence was

XX CC deduced from that of a cDNA clone (see AAV69277) isolated from a cardiac

XX CC coronary artery smooth muscle cell library. FTHMA-070 nucleic acids and

XX CC polypeptides of the invention are useful as modulating agents in

XX CC regulating a variety of cellular processes. They can be used for

CC identifying compounds which bind to or modulate the activity of the
CC polypeptides (claimed). They can also be used in screening assays,
CC detection assays (e.g. chromosomal mapping, tissue typing, forensic
CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials, and pharmacogenomics), and methods of
CC treatment (e.g. therapeutic and prophylactic) e.g. for neurological
CC disorders
XX

SQ Sequence 401 AA;

Query Match 87.2%; Score 1900; DB 2; Length 401;

Best Local Similarity 85.8%; Pred. No. 7, 2e-151;

Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLLDI-IEWTTOETLPPKYLHYDPTGHQLLCKDCAPGYLKHQCTVRRK 59

Db 1 MNKLLCCA-LVFLDISIKWTTQETPPKYLHYDEETSHQLLCKDCPPGYLKHQCTARWK 59

QY 60 TLVCPDHSYTDSTWHTSDVCYVSPVCKELQSVKQECNRTNHRVCECEGRYLEIEFCL 119

Db 60 TVCAPCPDHYTDSWHTSDVCLYVSPVCKELQVYKQECNRTNHRVCECEGRYLEIEFCL 119

QY 120 KHRSCPPGSGVQAGTPPERNTVCKCPDGFSSGETSSKAPCIKHNTCMSTFGLLLIQKNA 179

Db 120 KHRSCPPGSGVQAGTPPERNTVCKCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKNA 179

QY 180 THDNVCSGNREATQCGIDVTLCCEAFPRFAVPTKII PNWLSVLDLSLPGTKVNAESVER 239

Db 180 THDNICSGNSESTQCGIDVTLCCEAFPRFAVPTKFTPNWLSVLDNLPCTKVNAESVER 239

QY 240 IKRHSSQEQTFQLLKWKHQRNDQEWVKIIQDIDLCESSVQRHGHNLTEQLLALM 299

Db 240 IKRHSSQEQTFQLLKWKHQRNDQVVKIIQDIDLCESSVQRHGHNLTEQLLALM 299

QY 300 ESIPGKKISPEIERTRTKCKSEQLLKLKSLWRIKNGQDQTLKGLMYALKHLKTSHPFK 359

Db 300 ESIPGKKVGAEDIEKTIKACKPSDQILKLSLWRIKNGQDQTLKGLMHALKHKSHTYHPFK 359

RESULT 15

AAW83926

ID AAW83926 standard; protein; 401 AA.

XX AC AAW83926;

XX XX

XX DT 22-JAN-2001 (first entry)

XX DE A human tumour necrosis factor family receptor (TRI).

XX KW Human; tumour necrosis factor family receptor; TRI; tumour growth;

XX KW cell proliferation; chlamydia infection; immunodeficiency; septic shock;

XX KW T-cell mediated autoimmune disease; acquired immunodeficiency syndrome;

XX KW AIDS; cerebral malaria; graft rejection; cytotoxicity; cachexia;

XX KW apoptosis; inflammation; cancer; cardiovascular disease; angiogenesis;

XX KW inflammatory disease; atherosclerosis; diabetes mellitus; allergy;

XX KW neurological disorder; autoimmune disease; wound healing; bone formation;

XX KW osteoporosis.

XX OS Homo sapiens.

XX XX

XX FH Key

XX FT Peptide

XX FT Protein

XX FT

XX PN WO200054651-A2.

XX XX 21-SEP-2000.

XX PD

Location/Qualifiers

1..21 "signal peptide"

22..401

/note= "mature protein"


```
XX 15-MAR-2000; 2000WO-US0006592.
XX
XX 15-MAR-1999; 99US-0124489P.
XX 26-MAY-1999; 99US-0136248P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Greene JM, Fleischmann RD, Ni J;
XX WPI; 2000-618858/59.
XX DR N-PSDB; AAA75736.
XX
XX Novel tumor necrosis factor family receptor for diagnosing and treating
PT acquired immunodeficiency syndrome, cancer, cardiovascular diseases,
PT inflammatory diseases and autoimmune diseases.
XX
XX Claim 13; Fig 1A-B; 228pp; English.
XX
XX The present sequence represents a human tumour necrosis factor family
CC receptor (TR1) polypeptide. An agonist to the TR1 receptor is useful for
CC inhibiting tumour growth, to stimulate human cellular proliferation, to
CC regulate immune response and antiviral response, to protect against the
CC effects of ionising radiations, to protect against chlamydia infections,
CC to regulate growth, and to treat immunodeficiencies such as in human
CC immunodeficiency virus (HIV). An antagonist to the TR1 receptor is useful
CC for treating T-cell mediated autoimmune diseases, acquired
CC immunodeficiency syndrome (AIDS), septic shock, cerebral malaria, graft
CC rejection, cytotoxicity, cachexia, apoptosis, and inflammation. TR1
CC polynucleotides and polypeptides, and TR1 agonists and antagonists are
CC useful for treating cancers, cardiovascular diseases, inflammatory
CC diseases, atherosclerosis, diabetes mellitus, neurological disorders,
CC autoimmune diseases, for promoting angiogenesis, for treating allergy,
CC for wound healing, for regulating bone formation and for treating
XX osteoporosis
XX
XX Sequence 401 AA;
XX
Query Match 87.2%; Score 1900; DB 3; Length 401;
Best Local Similarity 85.8%; Pred. No. 7.2e-151;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;
QY 1 MNKWLCCALLVLDI-IEWTQETLPPKYLHYDPETHQQLLDCDCAPGYLKQHCTVRK 59
Db 1 MNKLLCCA-LVFLDISIKWTTQETLPPKYLHYDETSQQLLDCDCPPGYLKQHCTAKWK 59
QY 60 TLVCPGPDHSDYSDSWHTSDECVCSVCKELQSVQECNRTNRYCECEGRYLEIFCL 119
Db 60 TVCAPCPDHYTDSWHTSDECLYCSFVCKELQYVQECNRTNRYCECKEGRYLEIFCL 119
QY 120 KHRSPGPGSGVVOAGTPERTNVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLLIQKNA 179
Db 120 KHRSPGPGSGVVOAGTPERTNVCKKCPDGFSGETSSKAPCKHTNCSTFGLLLTOKNA 179
QY 180 THDNVCSGNREATKCGIDVTLCESAFRFAVPTKIIINWLSVLDLPGTKVNAESVER 239
Db 180 THDNVCSGNREATKCGIDVTLCESAFRFAVPTKIIINWLSVLDLPGTKVNAESVER 239
QY 240 IKRHSSQEQTFQLLKWQNRDQEMVKKIQQIDLCSSVQRHLGHSNLTTEOLLALM 299
Db 240 IKRHSSQEQTFQLLKWQNRDQEMVKKIQQIDLCSSVQRHLGHSNLTTEOLLALM 299
QY 300 ESLPGKKISPEIEIRTKYKSGSEQLKLLSLWRIKNGDQDTLKGLMYALKHKTSHFPK 359
Db 300 ESLPGKKVGAEDIEKTIKACPSDQILKLLSLWRIKNGDQDTLKGLMYALKHKTSHFPK 359
QY 360 TVTSHLRKTMRFHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
Db 360 TVTQSLKTIIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
```

Search completed: March 8, 2005, 14:38:14
Job time : 87.1064 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:28:42 ; Search time 21.9235 Seconds
(without alignments)
1365.399 Million cell updates/sec

Title: US-09-389-782A-2
Perfect score: 2179
Sequence: 1 MNKWLCCALLVLLDIIETWT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2179	100.0	401	3	US-08-974-022-4
2	2179	100.0	401	3	US-09-042-785A-13
3	2179	100.0	401	3	US-08-795-445A-4
4	2179	100.0	401	3	US-08-795-447A-4
5	2179	100.0	401	3	US-08-974-186-4
6	2179	100.0	401	3	US-08-795-446B-4
7	2179	100.0	401	3	US-08-706-945D-126
8	2179	100.0	401	4	US-08-577-788C-4
9	2179	100.0	401	4	US-08-577-788C-54
10	2079	95.4	401	3	US-08-974-022-2
11	2079	95.4	401	3	US-08-795-445A-2
12	2079	95.4	401	3	US-08-795-447A-2
13	2079	95.4	401	3	US-08-974-186-2
14	2079	95.4	401	3	US-08-795-446B-2
15	2079	95.4	401	3	US-08-706-945D-124
16	2079	95.4	401	4	US-08-577-788C-2
17	2079	95.4	401	4	US-08-577-788C-55
18	1955	89.7	364	3	US-08-706-945D-141
19	1900	87.2	401	3	US-09-153-927-1
20	1900	87.2	401	3	US-09-072-993C-1
21	1892	86.8	401	3	US-08-974-022-6
22	1892	86.8	401	3	US-09-042-785A-12
23	1892	86.8	401	3	US-08-795-445A-6
24	1892	86.8	401	3	US-08-795-447A-6
25	1892	86.8	401	3	US-08-974-186-6
26	1892	86.8	401	3	US-08-795-446B-6
27	1892	86.8	401	3	US-08-706-945D-128

28	1892	86.8	401	4	US-08-577-788C-6
29	1892	86.8	401	4	US-08-577-788C-56
30	1892	86.8	401	4	US-09-064-832-2
31	1727	79.3	364	3	US-08-706-945D-142
32	1427	65.5	293	4	US-09-896-096A-18
33	1128	51.8	208	4	US-08-577-788C-50
34	946	43.4	174	3	US-08-706-945D-136
35	838	38.5	161	4	US-09-632-277A-3
36	768	35.2	147	3	US-09-527-236A-20
37	768	35.2	147	4	US-09-527-236A-20
38	764	35.1	146	4	US-09-523-323-58
39	731	33.5	139	3	US-08-706-945D-130
40	424.5	19.5	271	4	US-09-936-019-1
41	424.5	19.5	300	2	US-08-794-796-2
42	424.5	19.5	300	4	US-09-632-277A-2
43	424.5	19.5	300	4	US-09-523-323-52
44	424.5	19.5	300	4	US-09-896-096A-1
45	424.5	19.5	300	4	US-09-936-019-3

ALIGNMENTS

RESULT 1
US-08-974-022-4
; Sequence 4, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behaviliand Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-4

Query Match 100.0%; Score 2179; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNKLCCALLVLLDIIETWTQTLPKYLHYDPETGHQLLCKCAPGTLYLKQHTVRRKT	60
DB	1	MNKLCCALLVLLDIIETWTQTLPKYLHYDPETGHQLLCKCAPGTLYLKQHTVRRKT	60
QY	61	LCVPCPDHSYTDSTWHTSDCVYCSVCKELQSVKQECNRTNHRVCEBGRYLEIFCLK	120

Db 61 LCVPCHSYTDSWHTSDECVYCSVPCKELQSVKQECNRTNHRVCEBGRYLEIEFCLK 120
Qy 121 HRSPPGSGVQAGTPERNTVCKKCPDGFSGFSETSKAPCIKHTNCSTFGLLIIOKGNAT 180
Db 121 HRSPPGSGVQAGTPERNTVCKKCPDGFSGFSETSKAPCIKHTNCSTFGLLIIOKGNAT 180
Qy 181 HDNVCNGREATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLDLPGTKVNAESVERI 240
Db 181 HDNVCNGREATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLDLPGTKVNAESVERI 240
Qy 241 KRRHSSQBOTFOLLKWKHONRDQEMVKII QIDIDLCSSVQRHGHSHNLTTQELLALME 300
Db 241 KRRHSSQBOTFOLLKWKHONRDQEMVKII QIDIDLCSSVQRHGHSHNLTTQELLALME 300
Qy 301 SLPGKKISPEEIERTRTKCSSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360
Db 301 SLPGKKISPEEIERTRTKCSSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360
Qy 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 2

US-09-042-785A-13
; Sequence 13, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-13

Query Match 100.0%; Score 2179; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLCDKCAPGTLYLKQHCCTVRRKT 60

Db 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLCDKCAPGTLYLKQHCCTVRRKT 60
Qy 61 LCVPCHSYTDSWHTSDECVYCSVPCKELQSVKQECNRTNHRVCEBGRYLEIEFCLK 120
Db 61 LCVPCHSYTDSWHTSDECVYCSVPCKELQSVKQECNRTNHRVCEBGRYLEIEFCLK 120
Qy 121 HRSPPGSGVQAGTPERNTVCKKCPDGFSGFSETSKAPCIKHTNCSTFGLLIIOKGNAT 180
Db 121 HRSPPGSGVQAGTPERNTVCKKCPDGFSGFSETSKAPCIKHTNCSTFGLLIIOKGNAT 180
Qy 181 HDNVCNGREATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLDLPGTKVNAESVERI 240
Db 181 HDNVCNGREATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLDLPGTKVNAESVERI 240
Qy 241 KRRHSSQBOTFOLLKWKHONRDQEMVKII QIDIDLCSSVQRHGHSHNLTTQELLALME 300
Db 241 KRRHSSQBOTFOLLKWKHONRDQEMVKII QIDIDLCSSVQRHGHSHNLTTQELLALME 300
Qy 301 SLPGKKISPEEIERTRTKCSSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360
Db 301 SLPGKKISPEEIERTRTKCSSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360
Qy 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 3

US-08-795-445A-4
; Sequence 4, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-445A-4

Query Match 100.0%; Score 2179; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLCDKCAPGTLYLKQHCCTVRRKT 60

Db 1 MNKWLCCALLVLLDIETWTTQETLPKYLHYDPETHGQLLCKDCAPGYLKQHCTVRRKT 60
QY 61 LCVPDPHSDVTSWHTSDECVYSPVKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
Db 61 LCVPDPHSDVTSWHTSDECVYSPVKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
QY 121 HRSPPGSGVQAGTVPERNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQGNAT 180
Db 121 HRSPPGSGVQAGTVPERNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQGNAT 180
QY 181 HDNVCSGNREATKCGIDVTLCCEAFPRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
Db 181 HDNVCSGNREATKCGIDVTLCCEAFPRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
QY 241 KRRHSSQEQTFQLLWKHQNDRQEMVKIIQIDILCESSVQRHLGHSNLTTEQLLALME 300
Db 241 KRRHSSQEQTFQLLWKHQNDRQEMVKIIQIDILCESSVQRHLGHSNLTTEQLLALME 300
QY 301 SLPGKKISPEIERTRTKCKSSBQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPPKT 360
Db 301 SLPGKKISPEIERTRTKCKSSBQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPPKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 4

US-08-795-447A-4
; Sequence 4, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-447A-4
Query Match 100.0%; Score 2179; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIETWTTQETLPKYLHYDPETHGQLLCKDCAPGYLKQHCTVRRKT 60
Db 1 MNKWLCCALLVLLDIETWTTQETLPKYLHYDPETHGQLLCKDCAPGYLKQHCTVRRKT 60

QY 61 LCVPDPHSDVTSWHTSDECVYSPVKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
Db 61 LCVPDPHSDVTSWHTSDECVYSPVKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
QY 121 HRSPPGSGVQAGTVPERNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQGNAT 180
Db 121 HRSPPGSGVQAGTVPERNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQGNAT 180
QY 181 HDNVCSGNREATKCGIDVTLCCEAFPRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
Db 181 HDNVCSGNREATKCGIDVTLCCEAFPRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
QY 241 KRRHSSQEQTFQLLWKHQNDRQEMVKIIQIDILCESSVQRHLGHSNLTTEQLLALME 300
Db 241 KRRHSSQEQTFQLLWKHQNDRQEMVKIIQIDILCESSVQRHLGHSNLTTEQLLALME 300
QY 301 SLPGKKISPEIERTRTKCKSSBQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPPKT 360
Db 301 SLPGKKISPEIERTRTKCKSSBQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPPKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 5

US-08-974-186-4
; Sequence 4, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPTROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/577,788
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-186-4
Query Match 100.0%; Score 2179; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIETWTTQETLPKYLHYDPETHGQLLCKDCAPGYLKQHCTVRRKT 60
Db 1 MNKWLCCALLVLLDIETWTTQETLPKYLHYDPETHGQLLCKDCAPGYLKQHCTVRRKT 60

Db 1 MNKWLCCALLVLLDIIIEWTTQETLPPKYLHYDPETGHQLLCKCAPGTYLKQHCIVRRKT 60
Qy 61 LCVPCPDHSYTDSDWHTSDCVYSPVKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
Db 61 LCVPCPDHSYTDSDWHTSDCVYSPVKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
Qy 121 HRSCPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
Db 121 HRSCPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
Qy 181 HDNVCNGREATOKGIDVTLCEEAFFRAVPTKIIIPNWSVLVDSLPGTKVNAESVERI 240
Db 181 HDNVCNGREATOKGIDVTLCEEAFFRAVPTKIIIPNWSVLVDSLPGTKVNAESVERI 240
Qy 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVORHLGHNSLTTEQLLAME 300
Db 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVORHLGHNSLTTEQLLAME 300
Qy 301 SLPGKKISPEETERTKTKSSEQLLKLWSLRINKGDDTLKGLMYALKHLKTSHPFKT 360
Db 301 SLPGKKISPEETERTKTKSSEQLLKLWSLRINKGDDTLKGLMYALKHLKTSHPFKT 360
Qy 361 VTHSLRKTMRFHLSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFHLSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 6

US-08-795-446B-4
; Sequence 4, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIORITY DATE:
; PRIOR APPLICATION DATA:
; FILING DATE: 08/577,788
; APPLICATION NUMBER: 08/577,788
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-446B-4

Query Match 100.0%; Score 2179; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKWLCCALLVLLDIIIEWTTQETLPPKYLHYDPETGHQLLCKCAPGTYLKQHCIVRRKT 60

Db 1 MNKWLCCALLVLLDIIIEWTTQETLPPKYLHYDPETGHQLLCKCAPGTYLKQHCIVRRKT 60
Qy 61 LCVPCPDHSYTDSDWHTSDCVYSPVKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
Db 61 LCVPCPDHSYTDSDWHTSDCVYSPVKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
Qy 121 HRSCPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
Db 121 HRSCPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
Qy 181 HDNVCNGREATOKGIDVTLCEEAFFRAVPTKIIIPNWSVLVDSLPGTKVNAESVERI 240
Db 181 HDNVCNGREATOKGIDVTLCEEAFFRAVPTKIIIPNWSVLVDSLPGTKVNAESVERI 240
Qy 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVORHLGHNSLTTEQLLAME 300
Db 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVORHLGHNSLTTEQLLAME 300
Qy 301 SLPGKKISPEETERTKTKSSEQLLKLWSLRINKGDDTLKGLMYALKHLKTSHPFKT 360
Db 301 SLPGKKISPEETERTKTKSSEQLLKLWSLRINKGDDTLKGLMYALKHLKTSHPFKT 360
Qy 361 VTHSLRKTMRFHLSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFHLSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 7

US-08-706-945D-126
; Sequence 126, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; CURRENT FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-706-945D-126

Query Match 100.0%; Score 2179; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKWLCCALLVLLDIIIEWTTQETLPPKYLHYDPETGHQLLCKCAPGTYLKQHCIVRRKT 60
Db 1 MNKWLCCALLVLLDIIIEWTTQETLPPKYLHYDPETGHQLLCKCAPGTYLKQHCIVRRKT 60
Qy 61 LCVPCPDHSYTDSDWHTSDCVYSPVKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
Db 61 LCVPCPDHSYTDSDWHTSDCVYSPVKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
Qy 121 HRSCPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
Db 121 HRSCPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180
Qy 181 HDNVCNGREATOKGIDVTLCEEAFFRAVPTKIIIPNWSVLVDSLPGTKVNAESVERI 240
Db 181 HDNVCNGREATOKGIDVTLCEEAFFRAVPTKIIIPNWSVLVDSLPGTKVNAESVERI 240
Qy 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVORHLGHNSLTTEQLLAME 300

Db 241 KRRHSSQEQTFQLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGLHNSLTTQQLALME 300
QY 301 SLPGKKISPEIERTRTKTCKSSBQLKLLSLWRIKNGDQDTLKLGLMYALKHLKTSHPPKT 360
Db 301 SLPGKKISPEIERTRTKTCKSSBQLKLLSLWRIKNGDQDTLKLGLMYALKHLKTSHPPKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 8

US-08-577-788C-4
; Sequence 4, Application US/08577788C
; Patent No. 6613544
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378 Rev
; CURRENT APPLICATION NUMBER: US/08/577,788C
; CURRENT FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-577-788C-4

Query Match 100.0%; Score 2179; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIEWTTQETLPPKYLHYDDETHGQLLCKDCAPGYLKQHCTVRRKT 60
Db 1 MNKWLCCALLVLDIIEWTTQETLPPKYLHYDDETHGQLLCKDCAPGYLKQHCTVRRKT 60
QY 61 LCVPCPDHSTYDSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
Db 61 LCVPCPDHSTYDSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
QY 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
Db 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
QY 181 HDNVCSGNREATOKCGIDVTLCBAAFRAVPTKIIIPNLSVLVDSIPLGTVKNAESVERI 240
Db 181 HDNVCSGNREATOKCGIDVTLCBAAFRAVPTKIIIPNLSVLVDSIPLGTVKNAESVERI 240
QY 241 KRRHSSQEQTFQLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGLHNSLTTQQLALME 300
Db 241 KRRHSSQEQTFQLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGLHNSLTTQQLALME 300
QY 301 SLPGKKISPEIERTRTKTCKSSBQLKLLSLWRIKNGDQDTLKLGLMYALKHLKTSHPPKT 360
Db 301 SLPGKKISPEIERTRTKTCKSSBQLKLLSLWRIKNGDQDTLKLGLMYALKHLKTSHPPKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 9

US-08-577-788C-54
; Sequence 54, Application US/08577788C
; Patent No. 6613544
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank

; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378 Rev
; CURRENT APPLICATION NUMBER: US/08/577,788C
; CURRENT FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 54
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-577-788C-54

Query Match 100.0%; Score 2179; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.3e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIEWTTQETLPPKYLHYDDETHGQLLCKDCAPGYLKQHCTVRRKT 60
Db 1 MNKWLCCALLVLDIIEWTTQETLPPKYLHYDDETHGQLLCKDCAPGYLKQHCTVRRKT 60
QY 61 LCVPCPDHSTYDSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
Db 61 LCVPCPDHSTYDSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
QY 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
Db 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
QY 181 HDNVCSGNREATOKCGIDVTLCBAAFRAVPTKIIIPNLSVLVDSIPLGTVKNAESVERI 240
Db 181 HDNVCSGNREATOKCGIDVTLCBAAFRAVPTKIIIPNLSVLVDSIPLGTVKNAESVERI 240
QY 241 KRRHSSQEQTFQLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGLHNSLTTQQLALME 300
Db 241 KRRHSSQEQTFQLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGLHNSLTTQQLALME 300
QY 301 SLPGKKISPEIERTRTKTCKSSBQLKLLSLWRIKNGDQDTLKLGLMYALKHLKTSHPPKT 360
Db 301 SLPGKKISPEIERTRTKTCKSSBQLKLLSLWRIKNGDQDTLKLGLMYALKHLKTSHPPKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 10

US-08-974-022-2
; Sequence 2, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:

```
;
;
; PRIORITY APPLICATION DATA:
; FILING DATE: 08/577,788
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-2

Query Match 95.4%; Score 2079; DB 3; Length 401;
Best Local Similarity 94.5%; Pred. No. 3e-186;
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIEWTTQETLPPKYLHYDPETGHQLLCKDCAPGTYLKQHCTVRRKT 60
Db 1 MNKWLCCALLVFLDIIEWTTQETLPPKYLHYDPETGRQLLCKDCAPGTYLKQHCTVRRKT 60
QY 61 LCVPCPDHSYTDSDHSTDECVYCSVKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
Db 61 LCVPCPDYSYTDSDHSTDECVYCSVKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
QY 121 HRCPPGSGVQAGTPERNTVCKKCPDGFSGTSSKAPCIKHTNGSTFGLLLIQKGNAT 180
Db 121 HRCPPGLGLVQAGTPERNTVCKKCPDGFSGTSSKAPCRKHTNCSSGLGLLIQKGNAT 180
QY 181 HDNVCSGNREATQCGIDVTLCCEAPFRFAVPTKIIIPNWLVSVDLPSTGKVAESVERI 240
Db 181 HDNVCSGNREATQCGIDVTLCCEAPFRFAVPTKIIIPNWLVSVDLPSTGKVAESVERI 240
QY 241 KRRHSSQEQTFQLLWKHQNDRQEMVKKIIQDIDLCESSVQRHGLHSNLTTEQLLAME 300
Db 241 KRRHSSQEQTFQLLWKHQNDRQEMVKKIIQDIDLCESSVQRHGLHSNLTTEQLRILME 300
QY 301 SLPGKKISPEIERTRKTKSSQELLKLSLWRKNGDQDTLKGMLYALKHLSHTSHFPKT 360
Db 301 SLPGKKISPEIERTRKTKSPSEQLLKLKSLWRKNGDQDTLKGMLYALKHLSHTSHFPKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEWIGNOVQSVKISCL 401
Db 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEWIGNOVQSVKISCL 401

RESULT 11
US-08-795-445A-2
; Sequence 2, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:

;
;
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; FILING DATE: 08/577,788
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-445A-2

Query Match 95.4%; Score 2079; DB 3; Length 401;
Best Local Similarity 94.5%; Pred. No. 3e-186;
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIEWTTQETLPPKYLHYDPETGHQLLCKDCAPGTYLKQHCTVRRKT 60
Db 1 MNKWLCCALLVFLDIIEWTTQETLPPKYLHYDPETGRQLLCKDCAPGTYLKQHCTVRRKT 60
QY 61 LCVPCPDHSYTDSDHSTDECVYCSVKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
Db 61 LCVPCPDYSYTDSDHSTDECVYCSVKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
QY 121 HRCPPGSGVQAGTPERNTVCKKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
Db 121 HRCPPGLGLVQAGTPERNTVCKKCPDGFSGTSSKAPCRKHTNCSSGLGLLIQKGNAT 180
QY 181 HDNVCSGNREATQCGIDVTLCCEAPFRFAVPTKIIIPNWLVSVDLPSTGKVAESVERI 240
Db 181 HDNVCSGNREATQCGIDVTLCCEAPFRFAVPTKIIIPNWLVSVDLPSTGKVAESVERI 240
QY 241 KRRHSSQEQTFQLLWKHQNDRQEMVKKIIQDIDLCESSVQRHGLHSNLTTEQLLAME 300
Db 241 KRRHSSQEQTFQLLWKHQNDRQEMVKKIIQDIDLCESSVQRHGLHSNLTTEQLRILME 300
QY 301 SLPGKKISPEIERTRKTKSSQELLKLSLWRKNGDQDTLKGMLYALKHLSHTSHFPKT 360
Db 301 SLPGKKISPEIERTRKTKSPSEQLLKLKSLWRKNGDQDTLKGMLYALKHLSHTSHFPKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEWIGNOVQSVKISCL 401
Db 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEWIGNOVQSVKISCL 401

RESULT 12
US-08-795-447A-2
; Sequence 2, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
```


;; FILING DATE: 514
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Winter, Robert B.
;; REFERENCE/DOCKET NUMBER: A-378D2
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 401 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-795-447A-2

Query Match 95.4%; Score 2079; DB 3; Length 401;
Best Local Similarity 94.5%; Pred. No. 3e-186;
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDDETHGQLLCKDCAPGTYLKQHCTVRRKT 60
DB 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDDETHGQLLCKDCAPGTYLKQHCTVRRKT 60
QY 61 LCVPCPDHSDYSDSWHTSDCYVSPVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
DB 61 LCVPCPDYSDYSDSWHTSDCYVSPVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
QY 121 HRSPPGSGVQAGTPERNTVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
DB 121 HRSPPGLGLVQAGTPERNTVCKCPDGFSGTSSKAPCRKHTNCSSGLGLLIQKGNAT 180
QY 181 HDNVCNREATOKCGIDVTLCEAEPFAVPPTKIIPNWLVLVDSIPGTVKNAESVERI 240
DB 181 HDNVCNREATONCGIDVTLCEAEPFAVPPTKIIPNWLVLVDSIPGTVKNAESVERI 240
QY 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKIIQDIDLCESSVQRHGHANLITTEQLRLME 300
DB 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKIIQDIDLCESSVQRHGHANLITTEQLRLME 300
QY 301 SLPGKISPEIERTRKTKCSSSEQLLKLWLRIKNGDQDTLKLGMVALKHLKTSHPKPT 360
DB 301 SLPGKISPEIERTRKTKCPSEQLLKLWLRIKNGDQDTLKLGMVALKHLKAYHPKPT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
DB 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 13
US-08-974-186-2
; Sequence 2, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; FILING DATE: 08/577,788
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Winter, Robert B.
;; REFERENCE/DOCKET NUMBER: A-378
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 401 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-974-186-2

Query Match 95.4%; Score 2079; DB 3; Length 401;
Best Local Similarity 94.5%; Pred. No. 3e-186;
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDDETHGQLLCKDCAPGTYLKQHCTVRRKT 60
DB 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDDETHGQLLCKDCAPGTYLKQHCTVRRKT 60
QY 61 LCVPCPDHSDYSDSWHTSDCYVSPVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
DB 61 LCVPCPDYSDYSDSWHTSDCYVSPVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
QY 121 HRSPPGSGVQAGTPERNTVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180
DB 121 HRSPPGLGLVQAGTPERNTVCKCPDGFSGTSSKAPCRKHTNCSSGLGLLIQKGNAT 180
QY 181 HDNVCNREATOKCGIDVTLCEAEPFAVPPTKIIPNWLVLVDSIPGTVKNAESVERI 240
DB 181 HDNVCNREATONCGIDVTLCEAEPFAVPPTKIIPNWLVLVDSIPGTVKNAESVERI 240
QY 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKIIQDIDLCESSVQRHGHANLITTEQLRLME 300
DB 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKIIQDIDLCESSVQRHGHANLITTEQLRLME 300
QY 301 SLPGKISPEIERTRKTKCSSSEQLLKLWLRIKNGDQDTLKLGMVALKHLKTSHPKPT 360
DB 301 SLPGKISPEIERTRKTKCPSEQLLKLWLRIKNGDQDTLKLGMVALKHLKAYHPKPT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
DB 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 14
US-08-795-446B-2
; Sequence 2, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:

; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/577,788
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Winter, Robert B.
 ; REFERENCE/DOCKET NUMBER: A-378
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 401 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-795-446B-2

Query Match 95.4%; Score 2079; DB 3; Length 401;
 Best Local Similarity 94.5%; Pred. No. 3e-186;
 Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60
 Db 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60
 QY 61 LCVPCPDHSYTDSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
 Db 61 LCVPCPDYSYTDSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
 QY 121 HRSCPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLIIQGNAT 180
 Db 121 HRSCPPGLGVLOAGTPERNTVCKCPDGFSGSETSSKAPCRKHTNCSSLGILLIIQGNAT 180
 QY 181 HDNVCSGNREATQKCGIDVTLCCEAFPRFAVPTKIIIPNWLSDLVDSLPQTKVNAESVERI 240
 Db 181 HDNVCSGNREATQNGCIDVTLCCEAFPRFAVPTKIIIPNWLSDLVDSLPQTKVNAESVERI 240
 QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGHNSLTTEQLLALME 300
 Db 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGHNSLTTEQLLALME 300
 QY 301 SLPCKKISPEIEIRTRKTCKSEQLLKLSLWRINKGDQDTLKGIMYALKHLKTSHPFKT 360
 Db 301 SLPCKKISPEIEIRTRKTCKSEQLLKLSLWRINKGDQDTLKGIMYALKHLKTSHPFKT 360
 QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
 Db 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 15

US-08-706-945D-124
 ; Sequence 124, Application US/08706945D
 ; Patent No. 6369027
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William
 ; APPLICANT: Lacey, David
 ; APPLICANT: Calzone, Frank
 ; APPLICANT: Chang, Ming-Shi
 ; TITLE OF INVENTION: Osteoprotegerin
 ; FILE REFERENCE: A-378CIP
 ; CURRENT APPLICATION NUMBER: US/08/706,945D
 ; PRIOR FILING DATE: 1996-09-03
 ; PRIOR APPLICATION NUMBER: 08/577,788
 ; PRIOR FILING DATE: 1995-12-22
 ; NUMBER OF SEQ ID NOS: 145
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 124
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Rattus rattus
 ; US-08-706-945D-124

Query Match 95.4%; Score 2079; DB 3; Length 401;
 Best Local Similarity 94.5%; Pred. No. 3e-186;

Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60
 Db 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60
 QY 61 LCVPCPDHSYTDSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
 Db 61 LCVPCPDYSYTDSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120
 QY 121 HRSCPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLIIQGNAT 180
 Db 121 HRSCPPGLGVLOAGTPERNTVCKCPDGFSGSETSSKAPCRKHTNCSSLGILLIIQGNAT 180
 QY 181 HDNVCSGNREATQKCGIDVTLCCEAFPRFAVPTKIIIPNWLSDLVDSLPQTKVNAESVERI 240
 Db 181 HDNVCSGNREATQNGCIDVTLCCEAFPRFAVPTKIIIPNWLSDLVDSLPQTKVNAESVERI 240
 QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGHNSLTTEQLLALME 300
 Db 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGHNSLTTEQLLALME 300
 QY 301 SLPCKKISPEIEIRTRKTCKSEQLLKLSLWRINKGDQDTLKGIMYALKHLKTSHPFKT 360
 Db 301 SLPCKKISPEIEIRTRKTCKSEQLLKLSLWRINKGDQDTLKGIMYALKHLKTSHPFKT 360
 QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
 Db 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

Search completed: March 8, 2005, 14:48:09
 Job time : 31.9235 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:44:50 ; Search time 60.5885 Seconds
(without alignments)
2177.757 Million cell updates/sec

Title: US-09-389-782a-2

Perfect score: 2179
Sequence: 1 MNKWLCCALLVLDIIETWT.....QKLFLFMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2179	100.0	401	10	US-09-389-782-2
2	2179	100.0	401	10	US-09-405-032-123
3	2079	95.4	401	10	US-09-405-032-121
4	2061	94.6	380	10	US-09-405-032-138
5	1900	87.2	401	13	US-10-066-209-1
6	1900	87.2	401	13	US-10-105-934-2
7	1900	87.2	401	13	US-10-164-592-2
8	1900	87.2	401	14	US-10-044-674-3
9	1900	87.2	401	14	US-10-322-673-5
10	1900	87.2	401	14	US-10-139-785-5
11	1900	87.2	401	17	US-10-895-676-2
12	1895	87.0	401	9	US-09-062-113-5
13	1895	87.0	401	14	US-10-183-091-1
14	1895	87.0	401	14	US-10-183-091-1

14	1895	87.0	401	14	US-10-364-045-1	Sequence 1, Appli
15	1895	87.0	401	14	US-10-232-858-5	Sequence 1, Appli
16	1895	87.0	401	15	US-10-377-076-1	Sequence 5, Appli
17	1895	87.0	401	16	US-10-785-109-5	Sequence 5, Appli
18	1895	87.0	401	16	US-10-785-114-5	Sequence 5, Appli
19	1895	87.0	401	17	US-10-929-958-5	Sequence 5, Appli
20	1895	87.0	401	17	US-10-929-748-5	Sequence 5, Appli
21	1892	86.8	401	10	US-09-405-032-125	Sequence 125, App
22	1892	86.8	401	14	US-10-151-071-8	Sequence 8, Appli
23	1892	86.8	401	16	US-10-467-243-2	Sequence 2, Appli
24	1892	86.8	401	17	US-10-129-595-3	Sequence 3, Appli
25	1897	86.6	400	14	US-10-142-658-2	Sequence 2, Appli
26	1885	86.5	401	9	US-09-062-113-62	Sequence 62, Appli
27	1885	86.5	401	9	US-09-062-113-63	Sequence 63, Appli
28	1885	86.5	401	9	US-09-062-113-65	Sequence 65, Appli
29	1885	86.5	401	9	US-09-062-113-66	Sequence 66, Appli
30	1885	86.5	401	14	US-10-232-858-62	Sequence 62, Appli
31	1885	86.5	401	14	US-10-232-858-63	Sequence 63, Appli
32	1885	86.5	401	14	US-10-232-858-64	Sequence 64, Appli
33	1885	86.5	401	14	US-10-232-858-65	Sequence 65, Appli
34	1885	86.5	401	14	US-10-232-858-66	Sequence 66, Appli
35	1885	86.5	401	16	US-10-785-109-62	Sequence 62, Appli
36	1885	86.5	401	16	US-10-785-109-63	Sequence 63, Appli
37	1885	86.5	401	16	US-10-785-109-64	Sequence 64, Appli
38	1885	86.5	401	16	US-10-785-109-65	Sequence 65, Appli
39	1885	86.5	401	16	US-10-785-109-66	Sequence 66, Appli
40	1885	86.5	401	16	US-10-785-114-62	Sequence 62, Appli
41	1885	86.5	401	16	US-10-785-114-63	Sequence 63, Appli
42	1885	86.5	401	16	US-10-785-114-64	Sequence 64, Appli
43	1885	86.5	401	16	US-10-785-114-65	Sequence 65, Appli
44	1885	86.5	401	16	US-10-785-114-66	Sequence 66, Appli
45	1885	86.5	401	16	US-10-785-114-66	Sequence 66, Appli

ALIGNMENTS

RESULT 1
US-09-389-782-2
; Publication No. US09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
; US-09-389-782-2

Query Match 100.0%; Score 2179; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.3e-171;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNKWLCCALLVLDIIETWTQETLPPKYLHYDPTGHLLCDKCAPGTYLKQHTVRRKT	60
Db	1	MNKWLCCALLVLDIIETWTQETLPPKYLHYDPTGHLLCDKCAPGTYLKQHTVRRKT	60
Qy	61	LCVPCPDHSYTSWHTSDSCVYCSVKELQSVKQCNRTHNRVCEBGRYLEIRFCLK	120
Db	61	LCVPCPDHSYTSWHTSDSCVYCSVKELQSVKQCNRTHNRVCEBGRYLEIRFCLK	120
Qy	121	HRSCPPGSGVQAGTPERNTVCKCPDGFSGTSSKAPCIKHTNCGSTFGLLIQKGNAT	180
Db	121	HRSCPPGSGVQAGTPERNTVCKCPDGFSGTSSKAPCIKHTNCGSTFGLLIQKGNAT	180

QY 181 HDNVCNREATQKCGIDVTLCEAFRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
DB 181 HDNVCNREATQKCGIDVTLCEAFRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300
DB 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300
QY 301 SLPGKKISPEIERTRKTKCSSEQLLKLSLWRINKGDDOTLKGLMYALKHLKTSHPFKT 360
DB 301 SLPGKKISPEIERTRKTKCSSEQLLKLSLWRINKGDDOTLKGLMYALKHLKTSHPFKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
DB 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
RESULT 2
US-09-405-032-123
; Sequence 123, Application US/09405032
; Publication No. US20030207827A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/405,032
; FILING DATE: 24-Sep-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Wintek, Robert B.
; REFERENCE/DOCKET NUMBER: A-378-CIP2
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-09-405-032-123
Query Match 100.0%; Score 2179; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.3e-171;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKCAPGTYLKHQCTVRRKT 60
DB 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKCAPGTYLKHQCTVRRKT 60
QY 61 LCVPCPDHSYTDSWHTSDSCVYCSVKELQSVKQECNRTNHRVCECEBGRYLEIEFCLK 120
DB 61 LCVPCPDHSYTDSWHTSDSCVYCSVKELQSVKQECNRTNHRVCECEBGRYLEIEFCLK 120
QY 121 HRSCTPGSGVGVQAGTPERTNVCCKPDGFFSGETSSKAPCIKHTNCSTFGLLIIQGNAT 180
DB 121 HRSCTPGSGVGVQAGTPERTNVCCKPDGFFSGETSSKAPCIKHTNCSTFGLLIIQGNAT 180
QY 181 HDNVCNREATQKCGIDVTLCEAFRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
DB 181 HDNVCNREATQKCGIDVTLCEAFRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240

QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300
DB 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300
QY 301 SLPGKKISPEIERTRKTKCSSEQLLKLSLWRINKGDDOTLKGLMYALKHLKTSHPFKT 360
DB 301 SLPGKKISPEIERTRKTKCSSEQLLKLSLWRINKGDDOTLKGLMYALKHLKTSHPFKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
DB 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
RESULT 3
US-09-405-032-121
; Sequence 121, Application US/09405032
; Publication No. US20030207827A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/405,032
; FILING DATE: 24-Sep-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Wintek, Robert B.
; REFERENCE/DOCKET NUMBER: A-378-CIP2
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 121:
US-09-405-032-121
Query Match 95.4%; Score 2079; DB 10; Length 401;
Best Local Similarity 94.5%; Pred. No. 5.9e-163;
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
QY 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKCAPGTYLKHQCTVRRKT 60
DB 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKCAPGTYLKHQCTVRRKT 60
QY 61 LCVPCPDHSYTDSWHTSDSCVYCSVKELQSVKQECNRTNHRVCECEBGRYLEIEFCLK 120
DB 61 LCVPCPDHSYTDSWHTSDSCVYCSVKELQSVKQECNRTNHRVCECEBGRYLEIEFCLK 120
QY 121 HRSCTPGSGVGVQAGTPERTNVCCKPDGFFSGETSSKAPCIKHTNCSTFGLLIIQGNAT 180
DB 121 HRSCTPGSGVGVQAGTPERTNVCCKPDGFFSGETSSKAPCIKHTNCSTFGLLIIQGNAT 180
QY 181 HDNVCNREATQKCGIDVTLCEAFRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
DB 181 HDNVCNREATQKCGIDVTLCEAFRFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240
QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300
DB 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300

QY 301 SLPKKISPEIRTRKTKSSBOLLKLLSLWRIKNGDQDTLGLMYALKHKTSHPEPKT 360
DB 301 SLPEKISPEIRTRKTKSPBOLLKLLSLWRIKNGDQDTLGLMYALKHKTSHPEPKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
DB 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 4

US-09-405-032-138
; Sequence 138, Application US/09405032
; Publication No. US20030207827A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Denavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/405,032
; FILING DATE: 24-Sep-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378-CIP2
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 138:
US-09-405-032-138

Query Match 94.6%; Score 2061; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.7e-161;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ETLPKYLHYDPETGHQLLCKCAPGTLYLKQHCTVRRKTLVCPDHSYTDSDWHTSDECY 81
DB 1 ETLPKYLHYDPETGHQLLCKCAPGTLYLKQHCTVRRKTLVCPDHSYTDSDWHTSDECY 60
QY 82 YCSFVKELQSVQECNRTHNRVCEBEGYLBIEFCLKRSPPGSGVVGAGTPEINTV 141
DB 61 YCSFVKELQSVQECNRTHNRVCEBEGYLBIEFCLKRSPPGSGVVGAGTPEINTV 120
QY 142 CKKCPDGFSGSTSSKAPCIKHTNCSTFGLLQKGNATHDNCVGNREATKCGIDVTL 201
DB 121 CKKCPDGFSGSTSSKAPCIKHTNCSTFGLLQKGNATHDNCVGNREATKCGIDVTL 180
QY 202 CEEAFFRFAVPTKIIPNWSLVDSLPFGTKVNAESVERIKRRHSSQEQTFQLLKLWKHQ 261
DB 181 CEEAFFRFAVPTKIIPNWSLVDSLPFGTKVNAESVERIKRRHSSQEQTFQLLKLWKHQ 240
QY 262 RDEWVKKIIQDIDLCSSVQRHLGHSNLTTEQLLALMESLPKKISPEIERTRKTKS 321
DB 241 RDEWVKKIIQDIDLCSSVQRHLGHSNLTTEQLLALMESLPKKISPEIERTRKTKS 300
QY 322 SEQLLKLSLWRIKNGDQDTLGLMYALKHKTSHPEPKT VTHSLRKTMRFLHSFTMYRLY 381
DB 301 SEQLLKLSLWRIKNGDQDTLGLMYALKHKTSHPEPKT VTHSLRKTMRFLHSFTMYRLY 360

QY 382 OKLFLEMIGNQVQSVKISCL 401
DB 361 OKLFLEMIGNQVQSVKISCL 380

RESULT 5

US-10-066-209-1
; Sequence 1, Application US/10066209
; Publication No. US20020115110A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; FILE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030-D1
; CURRENT APPLICATION NUMBER: US/10/066,209
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/072,993
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-10-066-209-1

Query Match 87.2%; Score 1900; DB 13; Length 401;
Best Local Similarity 85.8%; Pred. No. 3.5e-148;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLLDI-IETWTOETLPPKYLHYDPETGHQLLCKCAPGTLYLKQHCTVRRK 59
DB 1 MNKWLCCA-LVFLDISIKWTQTETPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWK 59
QY 60 TLCVPCPDHSYTDSDWHTSDECVYCSVCKELQSVQECNRTHNRVCEBEGYLBIEFCL 119
DB 60 TVCAPCPDHYTDSWHTSDECLYCSVCKELQSVQECNRTHNRVCEBEGYLBIEFCL 119
QY 120 KHRSCPPGSGVVGAGTPEINTVCKCPDGFSGSTSSKAPCIKHTNCSTFGLLQKGN 179
DB 120 KHRSCPPGSGVVGAGTPEINTVCKCPDGFSGSTSSKAPCIKHTNCSTFGLLQKGN 179
QY 180 THDNVCSGNREATKCGIDVTLCCEAFAFFRAVPTKIIPNWSLVDSLPKTKVNAESVER 239
DB 180 THDNVCSGNREATKCGIDVTLCCEAFAFFRAVPTKIIPNWSLVDSLPKTKVNAESVER 239
QY 240 IKRRHSSQEQTFQLLKLWKHQNDQEMVKIITQDIDLCSSVQRHLGHSNLTTEQLLALM 299
DB 240 IKRRHSSQEQTFQLLKLWKHQNDQEMVKIITQDIDLCSSVQRHLGHSNLTTEQLLALM 299
QY 300 ESLPGKKISPEIERTRKTKCSSEQLLKLWRIKNGDQDTLGLMYALKHKTSHPEPK 359
DB 300 ESLPGKKISPEIERTRKTKCSSEQLLKLWRIKNGDQDTLGLMYALKHKTSHPEPK 359
QY 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
DB 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 6

US-10-105-934-2
; Sequence 2, Application US/10105934
; Publication No. US20020150988A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.

Holtzman, Douglas
 TITLE OF INVENTION: NOVEL MOLECULES OF THE FTHMA-070-RELATED PROTEIN FAMILY AND THE T85-RELATED PROTEIN FAMILY AND USES THEREOF
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/105,934
 FILING DATE: 25-Mar-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/062,389
 FILING DATE: 17-APR-1998
 APPLICATION NUMBER: 60/062,017
 FILING DATE: 10-OCT-1997
 APPLICATION NUMBER: 60/044,746
 FILING DATE: 18-APR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 09404/051001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 401 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-105-934-2

Query Match 87.2%; Score 1900; DB 13; Length 401;
 Best Local Similarity 85.8%; Pred. No. 3.5e-148;
 Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;
 QY 1 MNKWLCCALLVLDDI-IEWTQETLPPKYLHYDPETGHQLLCKKCAPGTYLKQHCTVRRK 59
 DB 1 MNKLLCCA-LVFLDISIKWTTQETFPKYLHYDEETSHQLLCKKCPGPGTTLKQHCTAKWK 59
 QY 60 TLCVPCPDHSDYSDSWHTSDVCVSPVKELQSVKQECNTHNRVCECEGRYLEIEFCL 119
 DB 60 TVCAPCPDHYTDSWHTSDVCVSPVKELQSVKQECNTHNRVCECEGRYLEIEFCL 119
 QY 120 KHRSCPPGSGVQAGTPERTNTVCKCPDGFSGSTSKAPCIKHTNCSTFGLLLIQKNA 179
 DB 120 KHRSCPPGSGVQAGTPERTNTVCKCPDGFSGSTSKAPCRKHTNCSVFGLLLTQKNA 179
 QY 180 THDNVCSGNREATQKCGIDVTLCEEAFFFAVPTKIIIPNWLSDVSLPGTKVNAESVER 239
 DB 180 THDNVCSGNREATQKCGIDVTLCEEAFFFAVPTKIIIPNWLSDVSLPGTKVNAESVER 239
 QY 240 IKRRHSSQEQTFQLLKLWKHQNDRDQEMVKKIIQDIDLCSSVQRHGLHSNLTTEQLLALM 299
 DB 240 IKRRHSSQEQTFQLLKLWKHQNDRDQEMVKKIIQDIDLCSSVQRHGLHSNLTTEQLLALM 299
 QY 300 ESLPGKKISPEEIERTRKTSKSEQLLKLWLRIKNGDQDTLGLMYALKHLKTSHPFK 359
 DB 300 ESLPGKKVGAEDIEKTIKAKPSDQILKLLSLWRIKNGDQDTLGLMYALKHLKTSHPFK 359
 QY 360 TVTSHLRKTMRFHLSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
 DB 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

QY 360 TVTSHLRKTMRFHLSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
 DB 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
 RESULT 7
 US-10-164-592-2
 ; Sequence 2, Application US/10164592
 ; Publication No. US20020150989A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Greene, John M.
 ; APPLICANT: Fleischmann, Robert D.
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
 ; FILE REFERENCE: 1488.0710007
 ; CURRENT APPLICATION NUMBER: US/10/164,592
 ; PRIOR FILING DATE: 2002-06-10
 ; PRIOR APPLICATION NUMBER: US 08/469,637
 ; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: PCT/US95/03216
 ; PRIOR FILING DATE: 1995-03-15
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-164-592-2

Query Match 87.2%; Score 1900; DB 13; Length 401;
 Best Local Similarity 85.8%; Pred. No. 3.5e-148;
 Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;
 QY 1 MNKWLCCALLVLDDI-IEWTQETLPPKYLHYDPETGHQLLCKKCAPGTYLKQHCTVRRK 59
 DB 1 MNKLLCCA-LVFLDISIKWTTQETFPKYLHYDEETSHQLLCKKCPGPGTTLKQHCTAKWK 59
 QY 60 TLCVPCPDHSDYSDSWHTSDVCVSPVKELQSVKQECNTHNRVCECEGRYLEIEFCL 119
 DB 60 TVCAPCPDHYTDSWHTSDVCVSPVKELQSVKQECNTHNRVCECEGRYLEIEFCL 119
 QY 120 KHRSCPPGSGVQAGTPERTNTVCKCPDGFSGSTSKAPCIKHTNCSTFGLLLIQKNA 179
 DB 120 KHRSCPPGSGVQAGTPERTNTVCKCPDGFSGSTSKAPCRKHTNCSVFGLLLTQKNA 179
 QY 180 THDNVCSGNREATQKCGIDVTLCEEAFFFAVPTKIIIPNWLSDVSLPGTKVNAESVER 239
 DB 180 THDNVCSGNREATQKCGIDVTLCEEAFFFAVPTKIIIPNWLSDVSLPGTKVNAESVER 239
 QY 240 IKRRHSSQEQTFQLLKLWKHQNDRDQEMVKKIIQDIDLCSSVQRHGLHSNLTTEQLLALM 299
 DB 240 IKRRHSSQEQTFQLLKLWKHQNDRDQEMVKKIIQDIDLCSSVQRHGLHSNLTTEQLLALM 299
 QY 300 ESLPGKKISPEEIERTRKTSKSEQLLKLWLRIKNGDQDTLGLMYALKHLKTSHPFK 359
 DB 300 ESLPGKKVGAEDIEKTIKAKPSDQILKLLSLWRIKNGDQDTLGLMYALKHLKTSHPFK 359
 QY 360 TVTSHLRKTMRFHLSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
 DB 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 8
 US-10-044-674-3
 ; Sequence 3, Application US/10044674
 ; Publication No. US2003017510A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chew, Anne
 ; APPLICANT: Denton, R. Rex
 ; APPLICANT: Bieglecki, Karyn M
 ; APPLICANT: Nandabalan, Krishnan
 ; APPLICANT: Stephens, J. Claiborne
 ; TITLE OF INVENTION: HAPLOTYPES OF THE TNFRSF11B GENE
 ; FILE REFERENCE: TNFRSF11B_MWH-0001US (CIP)

```

; CURRENT APPLICATION NUMBER: US/10/044,674
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/18803
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-674-3

Query Match      87.2%; Score 1900; DB 14; Length 401;
Best Local Similarity 85.8%; Pred. No. 3.5e-148;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLLDI-IETWTTQETLPKYLHYDPETGHQLLCKDCAPGTYLKQHCTVRRK 59
DB 1 MNKWLCCA-LVFLDISIKWTTQETFPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWK 59
QY 60 TLCVPCPDHSDYSDSWHTSDVCVYCSVKELQSVKQECNTHNRVCEBGRYLEIBFCL 119
DB 60 TVCAPCPDHYTSDSWHTSDCLYCSVKELQSVKQECNTHNRVCEBGRYLEIBFCL 119
QY 120 KHRSCPPGSGVQAGTPERNVCKCPDGFSGSETSKAPCIKHTNGSTFGLLLIQKNA 179
DB 120 KHRSCPPGFGVQAGTPERNVCKCPDGFSGSETSKAPCRKHTNGSVFGLLLTQKNA 179
QY 180 THDNVCSGNREATQKCGIDVTLCEAFAFPVPTKIIPNWLSVLVDSLPGTKVNAESVER 239
DB 180 THDNICSGNSESQKCGIDVTLCEAFAFPVPTKFTFNWLSVLVDSLPGTKVNAESVER 239
QY 240 IKRHSSEQEOTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGLGHSNLTTEQLLALM 299
DB 240 IKQHSSEQEOTFOLLKWLKHQNRDQIVKKIIQDIDLCESSVQRHGHANLTTEQLRSLM 299
QY 300 ESLPGKKISPEETERTKTKSSBOLLKLSLWRIKNGDQDTLGLMYALKHLSHTFPK 359
DB 300 ESLPGKKVGAEDIEKTKACKPSDQILKLSLWRIKNGDQDTLGLMHALKHLSKTYHFPK 359
QY 360 TVTHSLRKTWRFHLSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
DB 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 9
US-10-322-673-5
; Sequence 5, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      87.2%; Score 1900; DB 14; Length 401;

US-10-322-673-5
; Sequence 5, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-5

Query Match      87.2%; Score 1900; DB 14; Length 401;

```


Best Local Similarity 85.8%; Pred. No. 3.5e-148;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;
QY 1 MNKLLCCALLVLDI-IETWTOETLPPKYLHYDPTGHQLLDCDCAPGTYLKQHCCTVRK 59
Db 1 MNKLLCCCA-LVFLDISIKWTQETFPKYLHYDETSQQLLDCDCPPGTYLKQHCCTAKWK 59
QY 60 TLVCPDPSHYTDSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEGRYLEIEFCL 119
Db 60 TVCACPDPHYTDSWHTSDECLYCSVCKELQYVQKQECNRTHNRVCECKEGRYLEIEFCL 119
QY 120 KHRSCPPGSGVVOAGTPERNVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQKNA 179
Db 120 KHRSCPPGFGVVOAGTPERNVCKCPDGFSGSETSSKAPCRKHTNCSVFGLLLTQKNA 179
QY 180 THDNVCSGNREATKCGIDVTLCEAFRFAVPTKIIIPNMLSVLVDLSLPGTKVNAESVER 239
Db 180 THDNICSGNSESTKCGIDVTLCEAFRFAVPTKFTPNMLSVLVDNLPGTKVNAESVER 239
QY 240 IKRRHSSQEQTFQLLKLWKHQNRDOEMVKIIQIDILCESSVQRHLGHSNLTTEQLLALM 299
Db 240 IKRQHSQEQTFQLLKLWKHQKQDQIVKKIIQIDILCENSQVRHIGHANLTTEQLRSLM 299
QY 300 ESLPGKKISPEIERTRTKCKSSQQLAKLISLWIKNGDQDTLGLMYALKHLSHTSPK 359
Db 300 ESLPGKKVGAEDIEKTIKACKPSQILKLSLWIKNGDQDTLGLMHALKHLSHTYHPK 359
QY 360 TVTSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
Db 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
RESULT 11
US-10-895-676-2
; Sequence 2, Application US/10895676
; Publication No. US20050032172A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; HOLZMAN, Douglas
; TITLE OF INVENTION: NOVEL MOLECULES OF THE FTHMA-070-RELATED PROTEIN FAMILY AND THE T85-RELATED PROTEIN FAMILY AND USES THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/895,676
; FILING DATE: 21-Jul-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/105,934
; FILING DATE: 25-Mar-2002
; APPLICATION NUMBER: US/09/062,389
; FILING DATE: 17-APR-1998
; APPLICATION NUMBER: 60/062,017
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/044,746
; FILING DATE: 18-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/051001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-895-676-2
Query Match 87.2%; Score 1900; DB 17; Length 401;
Best Local Similarity 85.8%; Pred. No. 3.5e-148;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;
QY 1 MNKLLCCALLVLDI-IETWTOETLPPKYLHYDPTGHQLLDCDCAPGTYLKQHCCTVRK 59
Db 1 MNKLLCCCA-LVFLDISIKWTQETFPKYLHYDETSQQLLDCDCPPGTYLKQHCCTAKWK 59
QY 60 TLVCPDPSHYTDSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEGRYLEIEFCL 119
Db 60 TVCACPDPHYTDSWHTSDECLYCSVCKELQYVQKQECNRTHNRVCECKEGRYLEIEFCL 119
QY 120 KHRSCPPGSGVVOAGTPERNVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQKNA 179
Db 120 KHRSCPPGFGVVOAGTPERNVCKCPDGFSGSETSSKAPCRKHTNCSVFGLLLTQKNA 179
QY 180 THDNVCSGNREATKCGIDVTLCEAFRFAVPTKIIIPNMLSVLVDLSLPGTKVNAESVER 239
Db 180 THDNICSGNSESTKCGIDVTLCEAFRFAVPTKFTPNMLSVLVDNLPGTKVNAESVER 239
QY 240 IKRRHSSQEQTFQLLKLWKHQNRDOEMVKIIQIDILCESSVQRHLGHSNLTTEQLLALM 299
Db 240 IKRQHSQEQTFQLLKLWKHQKQDQIVKKIIQIDILCENSQVRHIGHANLTTEQLRSLM 299
QY 300 ESLPGKKISPEIERTRTKCKSSQQLAKLISLWIKNGDQDTLGLMYALKHLSHTSPK 359
Db 300 ESLPGKKVGAEDIEKTIKACKPSQILKLSLWIKNGDQDTLGLMHALKHLSHTYHPK 359
QY 360 TVTSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
Db 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
RESULT 12
US-09-062-113-5
; Sequence 5, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
; TITLE OF INVENTION: the Proteins
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Teeta, Hurwitz & Thibeault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,113
FILING DATE: 17-APR-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FEB-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOORE, Ronda P.
REGISTRATION NUMBER: 44,244
REFERENCE/DOCKET NUMBER: FJN-060DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..380
OTHER INFORMATION: /note= "(OCIF protein)"
US-09-062-113-5

Query Match 87.0%; Score 1895; DB 9; Length 401;
Best Local Similarity 85.6%; Pred. No. 8.9e-148;
Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;
Qy 1 MNKWLCCALLVLDI-IEWTTOETLPKYLHYDPETHGOLLCDKCAPGTYLKQHCTVRRK 59
Db 1 MNLLCCA-LVFLDISIKWTTQETFPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWK 59
Qy 60 TLCVPCPDHSDYSDSWHTSDCVCSVPCKELQSVKQECNTHNRVCECEGRYLEIEFCL 119
Db 60 TVCAPCPDHYTDSWHTSDCLYCSVPCKELQYVQKQCNTHNRVCECEGRYLEIEFCL 119
Qy 120 KHRSCPPGSGVQAGTPERNTVCKCPDGFPSGTSKAPCIKHTNCSSTFGLLLIQGNA 179
Db 120 KHRSCPPGFGVQAGTPERNTVCKCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKNA 179
Qy 180 THDNVCSGNREATQKCGIDVTLCSEAFPRFAPVTKIIPNWLVLVDSLPGTKNAESVER 239
Db 180 THDNICSGNSESTQKCGIDVTLCSEAFPRFAPVTKIIPNWLVLVDSLPGTKNAESVER 239
Qy 240 IKRHSSEOETFOLLKWLKHQNRQEMVKIIQDIDLCSSVQRHLGHSNLTTEQLLALM 299
Db 240 IKRHSSEOETFOLLKWLKHQNKQDQIVKKIQQDIDLCNSVQRHIGHANLTFEQLASLM 299
Qy 300 ESLPGKKISPEIERTRKTCSSQLLKLSLMRIKNGDQDTLKGMLYALKHLSHTSPPK 359
Db 300 ESLPGKKVGAEDIEKTIKACKPSQILKLLSLMRIKNGDQDTLKGMLHAKHSKTYHFPK 359
Qy 360 TVTHSLKRTMRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
Db TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

Db 360 TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
RESULT 13
US-10-183-091-1
Sequence 1, Application US/10183091
Publication No. US20030045456A1
GENERAL INFORMATION:
APPLICANT: Yamamoto, Shinichi
APPLICANT: Okada, Junichi
APPLICANT: Kurihara, Ateushi
APPLICANT: Numazawa, Taku
APPLICANT: Kondo, Junichi Tenda, Eisuke
APPLICANT: Mochizuki, Shinichi
APPLICANT: Nishi, Hirotaka
APPLICANT: Miyazaki, Hideki
TITLE OF INVENTION: A complex comprising OCIF and polysaccharide
FILE REFERENCE: 02280/HG
CURRENT APPLICATION NUMBER: US/10/183,091
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: JP 2001-198985
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (-21)..(-1)
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat peptide
LOCATION: (+1)..(+380)
OTHER INFORMATION:
US-10-183-091-1

Query Match 87.0%; Score 1895; DB 14; Length 401;
Best Local Similarity 85.6%; Pred. No. 8.9e-148;
Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;
Qy 1 MNKWLCCALLVLDI-IEWTTOETLPKYLHYDPETHGOLLCDKCAPGTYLKQHCTVRRK 59
Db 1 MNLLCCA-LVFLDISIKWTTQETFPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWK 59
Qy 60 TLCVPCPDHSDYSDSWHTSDCVCSVPCKELQSVKQECNTHNRVCECEGRYLEIEFCL 119
Db 60 TVCAPCPDHYTDSWHTSDCLYCSVPCKELQYVQKQCNTHNRVCECEGRYLEIEFCL 119
Qy 120 KHRSCPPGSGVQAGTPERNTVCKCPDGFPSGTSKAPCIKHTNCSSTFGLLLIQGNA 179
Db 120 KHRSCPPGFGVQAGTPERNTVCKCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKNA 179
Qy 180 THDNVCSGNREATQKCGIDVTLCSEAFPRFAPVTKIIPNWLVLVDSLPGTKNAESVER 239
Db 180 THDNICSGNSESTQKCGIDVTLCSEAFPRFAPVTKIIPNWLVLVDSLPGTKNAESVER 239
Qy 240 IKRHSSEOETFOLLKWLKHQNRQEMVKIIQDIDLCSSVQRHLGHSNLTTEQLLALM 299
Db 240 IKRHSSEOETFOLLKWLKHQNKQDQIVKKIQQDIDLCNSVQRHIGHANLTFEQLASLM 299
Qy 300 ESLPGKKISPEIERTRKTCSSQLLKLSLMRIKNGDQDTLKGMLYALKHLSHTSPPK 359
Db 300 ESLPGKKVGAEDIEKTIKACKPSQILKLLSLMRIKNGDQDTLKGMLHAKHSKTYHFPK 359
Qy 360 TVTHSLKRTMRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
Db TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
RESULT 14
US-10-364-045-1

; Sequence 1, Application US/10364045
; Publication No. US20030139325A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Shinichi
; APPLICANT: Okada, Junichi
; APPLICANT: Kurihara, Acsuehi
; APPLICANT: Numazawa, Taku
; APPLICANT: Kondo, Junichi
; APPLICANT: Mochizuki, Shinichi
; APPLICANT: Nishi, Hirotsuka
; APPLICANT: Miyazaki, Hideki
; TITLE OF INVENTION: A complex comprising OCIF and polysaccharide
; FILE REFERENCE: 02280/HG
; CURRENT APPLICATION NUMBER: US/10/364,045
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US/10/183,091
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: JP 2001-198985
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (-21)..(-1)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (+1)..(+380)
; OTHER INFORMATION:
US-10-364-045-1

Query Match 87.0%; Score 1895; DB 14; Length 401;
Best Local Similarity 85.8%; Pred. No. 8.9e-148;
Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;
QY 1 MNKWLCCALLVLLDI - IEWTTQETLPKYLHYDPTGHQLCDKCAPGYLKQHCTVRRK 59
Db 1 MNLLCCA - LVFLDISIKWTQETFPKYLHYDEETSHQLCDKCPGGYLYLKQHCTAKWK 59
QY 60 TLVCPCPDHYSYDTSWHTSDECVYCSVKELQSVKQECNRTHNRVCECEGRLYEIEFCL 119
Db 60 TVCAPCPDHYTDSWHTSDECLYCSVKELQSVKQECNRTHNRVCECEGRLYEIEFCL 119
QY 120 KHRSCPPGSGVVOAGTPERTNVCCKCPDGFSGETSSKAPCIKHTNCSTFGILLITQKNA 179
Db 120 KHRSCPPGSGVVOAGTPERTNVCCKCPDGFSGETSSKAPCRKHTNCSTFGILLITQKNA 179
QY 180 THDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLVSVDLSLPGTKVNAESVER 239
Db 180 THDNICSGNSESTQKCGIDVTLCCEAFFRFAVPTKFTPNWLSVDNLPSTKVNAESVER 239
QY 240 IKRRHSSQEQTFQLLKLWKHQNRODMVKIIQDIDLCSSVQRHGHNSLNTTEQLLALM 299
Db 240 IKRQSSQEQTFQLLKLWKHQNRODMVKIIQDIDLCSSVQRHGHNSLNTTEQLRLSLM 299
QY 300 ESLPGKKISPEIERTRKTKSSQELLKLSLWRIKNGDQDTLKGIMVALKHLKTSHPFK 359
Db 300 ESLPGKKVGAEDIEKTIKACPSDQLLKLULSWRIKNGDQDTLKGIMVALKHLKTSHPFK 359
QY 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
Db 360 TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

Search completed: March 8, 2005, 15:16:01
Job time : 62.5885 secs

RESULT 15
US-10-232-858-5
; Sequence 5, Application US/10232858
; Publication No. US20030153048A1
; GENERAL INFORMATION:

; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20030153048A1uuyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20030153048A1uaki
; APPLICANT: MORNINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20030153048A1el Proteins and Methods for Producing the Prote
; FILE REFERENCE: 16991.004
; CURRENT APPLICATION NUMBER: US/10/232,858
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: PCT/JP96/00374
; PRIOR FILING DATE: 1996-02-20
; PRIOR APPLICATION NUMBER: 08/915,004
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-858-5

Query Match 87.0%; Score 1895; DB 14; Length 401;
Best Local Similarity 85.6%; Pred. No. 8.9e-148;
Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;
QY 1 MNKWLCCALLVLLDI - IEWTTQETLPKYLHYDPTGHQLCDKCAPGYLKQHCTVRRK 59
Db 1 MNLLCCA - LVFLDISIKWTQETFPKYLHYDEETSHQLCDKCPGGYLYLKQHCTAKWK 59
QY 60 TLVCPCPDHYSYDTSWHTSDECVYCSVKELQSVKQECNRTHNRVCECEGRLYEIEFCL 119
Db 60 TVCAPCPDHYTDSWHTSDECLYCSVKELQSVKQECNRTHNRVCECEGRLYEIEFCL 119
QY 120 KHRSCPPGSGVVOAGTPERTNVCCKCPDGFSGETSSKAPCIKHTNCSTFGILLITQKNA 179
Db 120 KHRSCPPGSGVVOAGTPERTNVCCKCPDGFSGETSSKAPCRKHTNCSTFGILLITQKNA 179
QY 180 THDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIIPNWLVSVDLSLPGTKVNAESVER 239
Db 180 THDNICSGNSESTQKCGIDVTLCCEAFFRFAVPTKFTPNWLSVDNLPSTKVNAESVER 239
QY 240 IKRRHSSQEQTFQLLKLWKHQNRODMVKIIQDIDLCSSVQRHGHNSLNTTEQLLALM 299
Db 240 IKRQSSQEQTFQLLKLWKHQNRODMVKIIQDIDLCSSVQRHGHNSLNTTEQLRLSLM 299
QY 300 ESLPGKKISPEIERTRKTKSSQELLKLSLWRIKNGDQDTLKGIMVALKHLKTSHPFK 359
Db 300 ESLPGKKVGAEDIEKTIKACPSDQLLKLULSWRIKNGDQDTLKGIMVALKHLKTSHPFK 359
QY 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
Db 360 TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:20:42 ; Search time 16.3429 Seconds
(without alignments)
2360.831 Million cell updates/sec

Title: US-09-389-782a-2
Perfect score: 2179
Sequence: 1 MNKWLCCALLVLDIIETWT.....QKLPLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	314	14.4	459	2 148854	gene murine tumor
2	312	14.3	461	1 A35356	tumor necrosis fac
3	312	14.3	474	2 B38634	tumor necrosis fac
4	300.5	13.8	651	2 JC7705	death receptor-6 -
5	270	12.4	305	2 A46476	B cell-associated
6	261	12.0	277	2 A60771	B-cell activation
7	244	11.2	435	2 I54182	tumor necrosis fac
8	233.5	10.7	325	2 B43692	T2 protein - rabbi
9	220	10.1	326	1 GQV2ML	T2 protein - myxom
10	217	10.0	349	2 D36858	gene G4R protein -
11	216	9.9	349	2 D72175	G2R protein - vari
12	215.5	9.9	348	2 T28623	hypothetical prote
13	199	9.1	427	1 GQHUN	nerve growth facto
14	197.5	9.1	425	1 A26431	nerve growth facto
15	184	8.4	416	1 JN0006	nerve growth facto
16	182	8.4	335	2 A40036	apoptosis-meditin
17	179.5	8.2	314	2 I37383	FAS soluble protei
18	177	8.1	256	2 B32393	T-cell antigen 4-1
19	167	7.7	255	2 I38426	lymphocyte activat
20	165.5	7.6	461	2 JC4302	tumor necrosis fac
21	163	7.5	271	2 S12783	OX40 antigen precu
22	161.5	7.4	454	1 GQMT1	tumor necrosis fac
23	160	7.3	465	1 GQHUT1	tumor necrosis fac
24	153	7.0	461	1 GQRT1	tumor necrosis fac
25	152.5	7.0	272	2 I48700	gene ox40 protein
26	151	6.9	272	2 I37552	OX40 homolog - hum
27	147.5	6.8	324	2 JC2395	Fas antigen precu
28	143	6.6	327	2 A46484	apoptosis-meditin
29	142.5	6.5	2823	2 F87908	protein T22A3.8 [1

30	142.5	6.5	2823	2 T23064	hypothetical prote
31	142.5	6.5	3102	2 T43291	laminin alpha chai
32	139	6.4	595	2 A42086	CD30 antigen precu
33	137.5	6.3	899	2 G02428	subtilisin-like pr
34	137.5	6.3	915	2 JC6148	subtilisin-like pr
35	133	6.1	1786	1 MMHUB1	laminin beta-1 cha
36	131.5	6.0	260	1 A46517	CD27 antigen precu
37	128.5	5.9	1252	2 S36016	occyet wall protei
38	128.5	5.9	1790	1 MMFPB1	laminin beta-1 cha
39	126.5	5.8	1548	2 S34583	serine proteinase
40	125	5.7	1680	2 A43434	furin (EC 3.4.21.7
41	122	5.6	1372	2 T25933	hypothetical prote
42	120.5	5.5	250	1 A49053	CD27 antigen precu
43	120.5	5.5	2918	2 A54105	fibrillin-2 precu
44	119.5	5.5	1639	1 MMFPB2	laminin gamma-1 ch
45	119	5.5	1364	2 T00250	MEGF2 protein - hu

ALIGNMENTS

RESULT 1

I48854
gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848; PMID:7873884
A;Accession: I48854
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: UNIPROT:Q62327; EMBL:X76401; NID:q433830; PIDN:CAA53981.1; PID:q43383;
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 14.4%; Score 314; DB 2; Length 459;
Best Local Similarity 34.6%; Pred. No. 3.7e-14;
Matches 66; Conservative 20; Mismatches 79; Indels 26; Gaps 4;

Qy	18	WTQETLPKYL--HYDPTGH-----QLLCKCAPGYLKQHCVTVRKTL	62
Db	2	WATGHTVPAQVVLTPYKPEPGYEQISQEYIDRKAQMCACKCPGQVYKHCNKTSDTV	61
Qy	63	VPCPDHSYTDSTWHTSDCYVSPVKELQSVKQECNRTNRCVCEEGRYLEIEF----	117
Db	62	ADCEASMYTQVMNQFRTCLSSSSCSSTQVETRACTQQRNVCAAGRYCALKTHSGSC	121
Qy	118	--CLKHRSPPGSGVQAGTPERTVCKCPDGFSGETSSKAPCIKHTNCSTFGLLLIQ	175
Db	122	RQCMRLSKCGPGFVASSRAPNGVLCACAPCTFSDTTSSTVDCRPHRCS----ILAI	177
Qy	176	KGNAHDNVCS 186	
Db	178	PGNASTDAVCA 188	

RESULT 2

A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A35356; A36475; A48416; A36007; A32666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, M.P.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-461 <SMI>
A:Cross-references: UNIPROT:P20333; GB:M32315; NID:G189185; PIDN:AAA59929.1; PID:G189186
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occurring
A:Reference number: A36475; MUID:91045991; PMID:2172983
A:Accession: A36475
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195, 'R', 197-461 <KOH>
A:Cross-references: GB:M55994; GB:M38549; NID:G339757; PIDN:AAA36755.1; PID:G339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690; PMID:1966549
A:Accession: A48416
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 23-461 <DEM>
A:Cross-references: GB:S63368; NID:G235648; PIDN:AAB19824.1; PID:G235649
R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration
A:Reference number: A36007; MUID:90349572; PMID:2166946
A:Accession: A36007
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEU>
A:Cross-references: GB:M35857; NID:G339751; PIDN:AAA63262.1; PID:G339752
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors
A:Reference number: A23666; MUID:91056048; PMID:2173696
A:Accession: A23666
A>Status: preliminary
A:Molecule type: protein
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOB>
R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: B35010
A>Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
R:Kunert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of the murine p75-TNF receptor
A:Reference number: I38094; MUID:95121934; PMID:7821811
A:Accession: I38094
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701
C:Genetics:
A:Gene: GDB:TNFR2
A:Cross-references: GDB:125914; OMIM:191191
A:Map position: 1p36.2-1p36.2
A:Introns: 26/3
A>Note: the list of introns is incomplete
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F:40-76/Domain: NGF receptor repeat homology <NG1>
F:78-119/Domain: NGF receptor repeat homology <NG2>
F:120-162/Domain: NGF receptor repeat homology <NG3>
F:164-201/Domain: NGF receptor repeat homology <NG4>
F:262-279/Domain: transmembrane #status predicted <TMN>
F:280-461/Domain: intracellular #status predicted <INT>
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 312; DB 1; Length 461;
Best Local Similarity 34.7%; Pred. No. 5.1e-14;
Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;
QY 8 ALLVLLDIIETTTQETLPPK--YLHYDPETGH-----QLLCDKCAFGTYLKQH 53
DB 9 ALAVGLEL--WAAAHALPAQVAFTFYAEPGSGTCLRLREYDQTQAMCCSKCPQOAHAKVF 66
QY 54 CTVRKTLVCPDPHSYVTDSDSWHTSDECVYSPVKCKELQSVKQECNTRNHRVCEEGEGRYL 113
DB 67 CTKTSVDVCDSCEDSTYTLQWNVPECLSCGSRCSQDVETQACTREQNRICTRCPGNYC 126
QY 114 EI-----EFLKHSRCPGSGVVOAGTPERTVCKKCPDGFPSGETSSKAPCIKHTNCS 167
DB 127 ALSKQEGCRLCAPLKRCPGFGVARPGTETSDVVVCKPCAPGTFSNTTSDICRPHQICN 186
QY 168 TFGLLLIQKGNATHNVCS 186
DB 187 VVAI-----PGNASMDAVCT 201
RESULT 3
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: B38634; A40254; S54816
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors
A:Reference number: A38634; MUID:91187885; PMID:1849278
A:Accession: B38634
A:Molecule type: mRNA
A:Residues: 1-474 <LEW>
A:Cross-references: UNIPROT:P25119; GB:M60469; NID:G199827; PIDN:AAA39752.1; PID:G199828
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenks, Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor
A:Reference number: A40254; MUID:91246168; PMID:1645445
A:Accession: A40254
A:Molecule type: mRNA
A:Residues: 1-474 <GOO>
A:Cross-references: GB:M60469; NID:G199827; PIDN:AAA39752.1; PID:G199828
R:Kisssonarhis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995
A:Description: Characterization of the promoter region of the murine p75-TNF receptor.
A:Reference number: S54816
A:Accession: S54816
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <KIS>
A:Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA60618.1; PID:9809044
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology
C:Keywords: cytokine receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F:40-77/Domain: NGF receptor repeat homology <NG1>
F:79-120/Domain: NGF receptor repeat homology <NG2>
F:166-203/Domain: NGF receptor repeat homology <NG4>
Query Match 14.3%; Score 312; DB 2; Length 474;
Best Local Similarity 34.3%; Pred. No. 5.3e-14;
Matches 70; Conservative 22; Mismatches 84; Indels 28; Gaps 5;
QY 5 LCCALLVLDDIETWTTQETLPPKYL--HYDPTGH-----QLLCDKCAFGTY 49
DB 6 LWALVFEQL--WATGHTVPAQVLTVPKPGVGCISQEVYDRKAQMCCKACPPGY 63
QY 50 LKQHCVTVRKTLVCPDPHSYVTDSDSWHTSDECVYSPVKCKELQSVKQECNTRNHRVCEEGE 109
DB 64 VKHFCNKTSDTVACDCEASMYTQVMNQFRTCLSCSSSTTDDQVETRACTKQNRVCA 123

```
QY 110 GRYLEIEF-----CLKHRCPPGSGVVOAGTPERTVCKKCPDGFSGETSKAPCIK 162
Db 124 GRVCAKTHSGRCQCNKSLCKGFGVASSRPNAGNVLCACAPGFTSTTSVDCRP 183
QY 163 HTNCSTFGLLIQKGNATHDNVCS 186
Db 184 HRICS-----ILAIPGNASTAVCA 203

RESULT 4
JC7705
A;Cross-references: UNIPROT:P27512; GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, E.A.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A;Reference number: A46515; MUID:93094586; PMID:1281194
A;Accession: A46515
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-287, 'LV' <GRI>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; NID:
A;Experimental source: BAUB/c, liver
A;Note: sequence extracted from NCBI backbone (NCBI:P:120357)
C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 12.4%; Score 270; DB 2; Length 305;
Best Local Similarity 34.5%; Pred. No. 2.5e-11;
Matches 57; Conservative 26; Mismatches 68; Indels 14; Gaps 5;

QY 27 KYLHYPETGHQLLCKCAPGYLYKHCTVRRKTLVCPDHSYTSWHTSDSC---VYC 83
Db 30 QYLH-DGQ-----CCDLCPGSGRLTSHCTALEKTQCHPCDSGFSQAMNREIRCHQHRHC 83
QY 84 SPVCKELQSVQECNRTHNRVCEBGRYL---EIEFCLKHRSRCPGSGVVOAGTTPERT 140
Db 84 EP--NOGLRVKKEGTAEISTVCTCKEGQHCTSKDCBACQAHTPCIPFGVGMWATETDT 141
QY 141 VCKKCPDGFSGETSSKAPCIKHTNCSTFGLLIQKGNATHDNVC 185
Db 142 VCHPCVPGFSGNQSSLFKCYPMTSCEDKNLEVLQKTSQTNVIC 186

RESULT 6
A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
A;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A;Reference number: S04460; MUID:89356608; PMID:2475341
A;Accession: S04460
A;Molecule type: mRNA
A;Residues: 1-277 <STA>
A;Cross-references: UNIPROT:P25942; EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A;Reference number: A60771; MUID:89093941; PMID:2463309
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
A;Gene: GDB:CD40
A;Cross-references: GDB:215268; OMIM:109535
A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <TM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Aen) (covalent) #status predicted
```

```
QY 110 GRYLEIEF-----CLKHRCPPGSGVVOAGTPERTVCKKCPDGFSGETSKAPCIK 162
Db 124 GRVCAKTHSGRCQCNKSLCKGFGVASSRPNAGNVLCACAPGFTSTTSVDCRP 183
QY 163 HTNCSTFGLLIQKGNATHDNVCS 186
Db 184 HRICS-----ILAIPGNASTAVCA 203

RESULT 4
JC7705
A;Cross-references: UNIPROT:P27512; GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, E.A.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A;Reference number: A46515; MUID:93094586; PMID:1281194
A;Accession: A46515
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-287, 'LV' <GRI>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; NID:
A;Experimental source: BAUB/c, liver
A;Note: sequence extracted from NCBI backbone (NCBI:P:120357)
C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 12.4%; Score 270; DB 2; Length 305;
Best Local Similarity 34.5%; Pred. No. 2.5e-11;
Matches 57; Conservative 26; Mismatches 68; Indels 14; Gaps 5;

QY 27 KYLHYPETGHQLLCKCAPGYLYKHCTVRRKTLVCPDHSYTSWHTSDSC---VYC 83
Db 30 QYLH-DGQ-----CCDLCPGSGRLTSHCTALEKTQCHPCDSGFSQAMNREIRCHQHRHC 83
QY 84 SPVCKELQSVQECNRTHNRVCEBGRYL---EIEFCLKHRSRCPGSGVVOAGTTPERT 140
Db 84 EP--NOGLRVKKEGTAEISTVCTCKEGQHCTSKDCBACQAHTPCIPFGVGMWATETDT 141
QY 141 VCKKCPDGFSGETSSKAPCIKHTNCSTFGLLIQKGNATHDNVC 185
Db 142 VCHPCVPGFSGNQSSLFKCYPMTSCEDKNLEVLQKTSQTNVIC 186

RESULT 6
A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
A;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A;Reference number: S04460; MUID:89356608; PMID:2475341
A;Accession: S04460
A;Molecule type: mRNA
A;Residues: 1-277 <STA>
A;Cross-references: UNIPROT:P25942; EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A;Reference number: A60771; MUID:89093941; PMID:2463309
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
A;Gene: GDB:CD40
A;Cross-references: GDB:215268; OMIM:109535
A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <TM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Aen) (covalent) #status predicted
```

Query Match 12.0%; Score 261; DB 2; Length 277;
 Best Local Similarity 33.9%; Pred. No. 9.2e-11;
 Matches 58; Conservative 23; Mismatches 74; Indels 16; Gaps 4;

QY 29 LHYDPETG-----HQLLCKKAPGYLKQHTVRRKTLVCPDHPHSYTDHSHHTSDEC 80
 DB 18 VHEPPTACRKQVLIINSQCSLQPOGQKLVSDCTETETELCPGSESEFLDTWNRTHC 77
 QY 81 ---VYCSVPVKELQSVKQECNRTNHRVCEBEGRYL---EIEFCLKHSRCPGSGVVOAG 134
 DB 78 HOHKYCDNLG--LRVQKGTSEDTTCTCEGHCTSEACESVILHRSRCPGSGVVOAG 135
 QY 135 TPERNTVCKCPDPPFSGSETSSKAPCIKHTNCSTFGLLLIQGNATHDNVC 185
 DB 136 TGVSDTICEPCVPGVFFSNVSAFEKHPWTSCETKDLVQVQAGTKNDVVC 186

RESULT 7
 154182
 tumor necrosis factor receptor 2-related protein - human
 C:Species: Homo sapiens (man)
 C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
 C:Accession: I54182
 R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
 Genomics 16, 214-218, 1993
 A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
 A:Reference number: I54182; MUID:93252381; PMID:8486360
 A:Accession: I54182
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-435 <RES>
 A:Cross-references: UNIPROT:P36941; GB:I04270; NID:G339761; PIDN:AAA36757.1; PID:G339762
 C:Genetics:
 A:Gene: GDB:LTER
 A:Cross-references: GDB:1230195; OMIM:600979
 A:Map position: 12p13.3-12p13.1
 C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo

Query Match 11.2%; Score 244; DB 2; Length 435;
 Best Local Similarity 26.9%; Pred. No. 2.2e-09;
 Matches 54; Conservative 32; Mismatches 93; Indels 22; Gaps 6;

QY 9 LLVLLDIIEWTTQETLPP-----KYLHYDPETGHTQLLCKKAPGYLKQHTVRR 57
 DB 18 VLGLFGLLAASQOAVPPVASENQTCDQEKYEIEPQ--HRICCSKCPPTVTSKACSR 75
 QY 58 RKTLCVCPDHPHSYTDHSHHTSDECYCSVPVKELQSVKQ--ECNRTNHRVCEBEGRYL--- 112
 DB 76 RDTVCATCAENSYNHWNVLTICQLCRP--CDPVMGLEETAPCTSKRKTCRCQPGMFCNA 134
 QY 113 --LEIEFCLKHSRCPGSG--GVVQAGTPERTVCKCPDPPFSGSETSSKAPCIKHTNCSTF 169
 DB 135 WALECTHCLLSDCPPGTAEALKDEVGKGNHCVCPKAGHFQNTSSPSARCQPHTRCENQ 194
 QY 170 GLLLIQGNATHDNVCSGNRE 190
 DB 195 GLVERAPGTAQSDTTCKNPLE 215

RESULT 8
 B43692
 T2 protein - rabbit fibroma virus
 C:Species: rabbit fibroma virus, Shope fibroma virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: B43692
 R:Upton, C.; DeLange, A.M.; McFadden, G.
 Virology 160, 20-30, 1987
 A:Title: Tumorigenic poxviruses: Genomic organization and DNA sequence of the telomeric
 A:Reference number: A43692; MUID:87321103; PMID:2820128
 A:Accession: B43692
 A>Status: preliminary
 A:Molecule type: DNA

Query Match 10.7%; Score 233.5; DB 2; Length 325;
 Best Local Similarity 31.7%; Pred. No. 8.5e-09;
 Matches 59; Conservative 19; Mismatches 91; Indels 17; Gaps 5;

QY 36 GHQ-----LLCDKCAPGYLYKQHTVRRKTLVCPDHPHSYTDHSHHTSDECYCSVPVKEL 90
 DB 30 GHDEKDGCLCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHAPACVSCRGPCTGH 89
 QY 91 QSVKQECNRTNHRVCEBEGRYLEIE-----FCLKHSRCPGSGVVOAGTPERTVCKK 144
 DB 90 LSESQPCDRTHDRVCNCSGTNGYCLLKQNGCRICAPQTKCPAGY--VSGHTRAGDTLCEK 148
 QY 145 CPDPPFSGSETSSKAPCIKHTNCSTFGLLLIQGNATHDNVCSGNREATQKCGIDVTL--- 201
 DB 149 CPHHTYSDLSLPTERCCTGTSFNVISVGFNLYPV-NETSCTTAGHNEVIKTEFTVTLNVT 207
 QY 202 -CEEAP 206
 DB 208 DCDPVE 213

RESULT 9
 QGVZML
 T2 protein - myxoma virus (strain Lausanne)
 C:Species: myxoma virus
 C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C:Accession: A40566
 R:Upton, C.; Macen, J.L.; Schreiber, M.; McFadden, G.
 Virology 184, 370-382, 1991
 A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis fa
 A:Reference number: A40566; MUID:91335768; PMID:1651597
 A:Accession: A40566
 A:Molecule type: DNA
 A:Residues: 1-326 <UPT>
 A:Cross-references: UNIPROT:P29825; GB:M95181; GB:M37976; NID:G332309; PIDN:AAA46632.1; I
 C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
 C:Keywords: glycoprotein
 F:64-105/Domain: NGF receptor repeat homology <NG2>
 F:106-147/Domain: NGF receptor repeat homology <NG3>
 F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.1%; Score 220; DB 1; Length 326;
 Best Local Similarity 29.1%; Pred. No. 7.2e-08;
 Matches 53; Conservative 24; Mismatches 85; Indels 20; Gaps 5;

QY 39 LLCDCAPGYLYKQHTVRRKTLVCPDHPHSYTDHSHHTSDECYCSVPVKELQSVKQECN 98
 DB 38 LCCTSCPPGSVASRLCGPGSDTVCSPCNFTFTASTNHAPACVSCRGRCTGHLESQSD 97
 QY 99 RTHNRVCEBEGRYLEIE-----FCLKHSRCPGSGVVOAGTPERTVCKCPDPPFSG 152
 DB 98 KTRDRVCDCSAGNYCLLKQEGCRICAPKTKCPAGY--VSGHTRTGDLVLTCKPRYVSD 156
 QY 153 ETSSKAPCIKHTNCSTFGLLLIQG-----NATHDNVCSGNREATQKCGIDVTL----CEE 204
 DB 157 AVSTETC-----TSSFNYISVFNLYPVNDTCTTTAGPNEVVKTSEFSTVTLNHTDCDP 211
 QY 205 AF 206
 DB 212 VF 213

RESULT 10
 D36858
 gene G4R protein - variola virus
 N:Alternate names: B28R protein (COP)
 C:Species: variola virus

G2R protein - variola minor virus (strain Garcia-1966)

QY 31 YDPETG-----HQLLCDKCAPGTYLKQHCTVRRKTLCPDHSYTDSWHTSDEC V 81

Db 24 YTPNGKCKDTEYKRNLCCLSPGPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACL 83
QY 82 YCSPVCKELQVQKQECNTHNRVCEBEGRYLEI-----EFCLEKHSRPPGSGVVOAGT 135
Db 84 SCNGRCNSQVFRSCNTHNRICEGSPGYCLLKSSGCKACVQTKGIGVG-VSGHT 142
QY 136 PERNTVCKCPDGFPGFSGTSSKAPCIKHNCSTFGLLIQ-KGNATHDNVCSGNREATOK 194
Db 143 SVGDVICSPPCGFTYSHVTSADKCEPVFN-NTFNVIDVEITLYPVNDTSCT-----RTTT 197
QY 195 CGIDVTLCBEAFRFAVPYKIIIPWLVSLVDSLPFGTKVAESVERIKRRHSS-----REQ 249
Db 198 TGLSE-----SILTSEL-----TITMHTDCNPVREE 225
QY 250 TFOCLK-----LWKHQRNDQEMVKKIIQIDILCESSVORHLGHSNLTTEQLLALMESLP 303
Db 226 YFSVLNKAIVATSGFTGENRYONISK-----VCLTNFELKCNKSSPKQLTKAKND-- 276
QY 304 GKKSIPPEIERTKTKCSSEQLKLSLWRIKNGDDOTLKGLMYALKHL--KTSHP-- 358
Db 277 DGMMSHSETVTLAGDCLSSVDIYLSNTNAQDYETDTIS---YRVGNVLDDDDSHMPGSC 333
QY 359 ---KTVTHSLRKTMREL 372
Db 334 NIHKPITNS--KPTREL 348

RESULT 13
GOHUN
nerve growth factor receptor precursor, low affinity [validated] - human
N:Alternate names: NGF receptor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
R:Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A:Title: Expression and structure of the human NGF receptor.
A:Reference number: A25218; MUID:87051725; PMID:3022937
A:Accession: A25218
A:Molecule type: mRNA
A:Residues: 1-427 <JOH>
A:Cross-references: UNIPROT:P08138; GB:M14764; PIDN:AAB59544.1; PID:g189205
R:Marano, N.; Dietschold, B.; Earley Jr., J.J.; Schattman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
A:Reference number: A60204; MUID:87085574; PMID:3025363
A:Accession: A60204
A:Molecule type: protein
A:Residues: 29-31, 'T', 33-42, 'TT', 45-46, 'TX', 50-51, 'XX', 54-56 <MAR>
A:Experimental source: melanoma cell line A875
A:Note: This sequence has been corrected by a note added in proof to follow the nucleotide
R:Vissavajjala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A:Title: Structural domains of the extracellular domain of human nerve growth factor
A:Reference number: S21689; MUID:92198017; PMID:1372492
A:Accession: S21689
A>Status: preliminary
A:Molecule type: protein
A:Residues: 183-208 <VIS>
R:Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A:Title: A constitutive promoter directs expression of the nerve growth factor receptor
A:Reference number: I57638; MUID:89096903; PMID:2850481
A:Accession: I57638
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates w
C:Comment: This receptor undergoes both N- and O-linked glycosylation.

C:Genetics:
A:Gene: GDB:NGFR
A:Cross-references: GDB:120234; OMIM:162010
A:Map position: 17q21-17q22
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-427/Product: nerve growth factor receptor #status experimental <MAT>
F:32-65/Domain: extracellular #status predicted <EXT>
F:67-108/Domain: NGF receptor repeat homology <NG1>
F:109-147/Domain: NGF receptor repeat homology <NG2>
F:149-189/Domain: NGF receptor repeat homology <NG3>
F:197-248/Region: serine/threonine-rich
F:251-272/Domain: transmembrane #status predicted <TRM>
F:273-427/Domain: intracellular #status predicted <INT>
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 9.1%; Score 199; DB 1; Length 427;
Best Local Similarity 31.7%; Pred. No. 2.7e-06;
Matches 52; Conservative 25; Mismatches 71; Indels 16; Gaps 6;
QY 9 LILVLDITLWTTQETLPPKYLHYDBETHQLLCKDCAPGYLKQHTVRRKTLVCVCPDH 68
Db 17 LLLLLGSLGSGAKACPTGLYTHSGE-----CCKACNLGEGVAQPCGA-NQTVCEPCLDS 70
QY 69 -SYTDSWHTSDCVYCSVPCKELQSVKQECNTHNRVCEBEGRYLE-----IEFCLKHR 122
Db 71 VTFSDVVSNTPECKPCTE-CVGLQSMSPAPCVADDAVCECAYGYQDETTGRCEAC---R 126
QY 123 SCPGSGVVOAGTTPERTVCKCPDGFPGFSGTSSKAPCIKHNC 166
Db 127 VCEAGSLVFCQDKQNTVCBPCDGTYSDEANHVDPCLPCTVC 170

RESULT 14
A26431
nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A26431; PHI229
R:Kadeke, M.J.; Misko, T.P.; Hsu, C.; Herzberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115859; PMID:3027580
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
A:Cross-references: UNIPROT:P07174; GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756
R:Metzsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoic
A:Reference number: PHI229; MUID:93077038; PMID:1446821
A:Accession: PHI229
A:Molecule type: DNA
A:Residues: 1-20 <MET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates w
C:Genetics:
A:Introns: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-425/Product: nerve growth factor receptor #status predicted <EXT>
F:33-66/Domain: NGF receptor repeat homology <NG1>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-148/Domain: NGF receptor repeat homology <NG3>
F:150-190/Domain: NGF receptor repeat homology <NG4>
F:198-249/Region: serine/threonine-rich

```

F;24-57/Domain: NGF receptor repeat homology <NG1>
F;59-100/Domain: NGF receptor repeat homology <NG2>
F;101-139/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NG4>
F;189-237/Region: serine/threonine-rich
F;240-261/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      8.4%; Score 184; DB 1; Length 416;
Best Local Similarity 30.9%; Pred. No. 2.8e-05;
Matches 46; Conservative 28; Mismatches 67; Indels 8; Gaps 6;

Qy      41  CDKCAPGTVLKQHTVRRRLTLCVPCPDH--SYTDSMHTSDECVYCSVPCKELQSVKQECNR 99
Db      36  CKACNLGEGVVPQGV-NQTVCEPCLDSTVYSATSPCKPCTQ-CVGLHSMSPCVE 93

Qy      100 THNRVCEBEGRYLEIEF---CLKHRSCPPGGVGVOAGTPERNTVCKCPDGFSGETSS 156
Db      94  SDDAVCRAYG-YFDELSGSKCEKICEVGFGLMEPCRDSQDTVCECPEGTFSDANF 152

Qy      157 KAPCIKHTNCSTFGLLLIQGNATHDNVC 185
Db      153 VDPCLPCTICEB-NEVMVKECTATSDAEC 180

Search completed: March 8, 2005, 14:46:11
Job time : 26.3429 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:56 ; Search time 74.1412 Seconds
(without alignments)
2769.633 Million cell updates/sec

Title: US-09-389-782a-2
Perfect score: 2179
Sequence: 1 MNKWLCCALLVLDIIEWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2179	100.0	401	1 T11B MOUSE	O08712 mus musculus
2	2159	99.1	401	2 Q6P1I2	Q6P1I2 mus musculus
3	2079	95.4	401	1 T11B RAT	O08727 rattus norv
4	1900	87.2	401	1 T11B HUMAN	O00300 homo sapien
5	1014	46.5	387	2 Q6GLN3	Q6GLN3 xenopus lae
6	541	24.8	146	2 Q7ZZV4	Q7ZZV4 gallus gall
7	428	19.6	186	2 Q7ZZY5	Q7ZZY5 gallus gall
8	424.5	19.5	300	1 TR6B HUMAN	O95407 homo sapien
9	397.5	18.2	286	2 Q6NM61	Q6NM61 brachydanio
10	390.5	17.9	302	2 Q9PUS0	Q9PUS0 salvelinus
11	390	17.9	285	2 Q90W71	Q90W71 oncorhynch
12	383	17.6	285	2 Q90Y86	Q90Y86 oncorhynch
13	314	14.4	459	2 Q6Z3Z7	Q6Z3Z7 mus musculus
14	312	14.3	461	1 TR1B HUMAN	P20333 h tumor nec
15	312	14.3	474	1 TR1B MOUSE	P25119 mus musculus
16	301.5	13.8	655	1 TR21 HUMAN	O75509 homo sapien
17	301	13.8	461	2 Q6VAU8	Q6VAU8 rattus norv
18	301	13.8	474	1 TR1B RAT	Q80WY6 rattus norv
19	300.5	13.8	651	2 Q98SM6	Q98SM6 gallus gall
20	288	13.2	655	1 TR21 MOUSE	Q9EUP5 mus musculus
21	281	12.9	433	2 Q91ZM6	Q91ZM6 rattus norv
22	270	12.4	289	1 TNR5 MOUSE	P27512 mus musculus
23	270	12.4	289	2 Q8K2X6	Q8K2X6 mus musculus
24	268.5	12.3	467	2 Q800I0	Q800I0 gallus gall
25	268.5	12.3	625	1 TR11 MOUSE	Q35305 mus musculus
26	266.5	12.2	616	1 TR11 HUMAN	Q9Y6G6 homo sapien
27	266	12.2	462	2 Q805B0	Q805B0 gallus gall
28	263	12.1	457	2 Q81VS6	Q81VS6 homo sapien
29	263	12.1	483	2 Q80OK7	Q80OK7 paralicthy
30	261	12.0	223	2 Q86YK5	Q86YK5 homo sapien
31	261	12.0	277	1 TNR5 HUMAN	P25942 homo sapien

32	254.5	11.7	318	2	Q7T2H3	Q7T2H3 oncorhynch
33	249	11.4	169	2	Q9JKE0	Q9JKE0 rattus norv
34	248	11.4	276	2	Q9DDD2	Q9DDD2 gallus gall
35	247.5	11.4	275	2	Q80WM9	Q80WM9 mus musculus
36	247.5	11.4	276	2	Q71F55	Q71F55 mus musculus
37	244	11.2	435	1	TNR3 HUMAN	P36941 homo sapien
38	243	11.2	278	2	Q8SQJ4	Q8SQJ4 sus scrofa
39	235	10.8	274	2	Q7YRL5	Q7YRL5 canis famlil
40	233.5	10.7	325	1	VT2 SFVKA	P25943 shope fibro
41	233.5	10.7	325	2	Q77PB3	Q77PB3 rabbit fibr
42	229	10.5	277	2	Q8WMQ2	Q8WMQ2 ovis aries
43	228	10.5	269	1	TNR5 BOVIN	Q28203 bos taurus
44	226	10.4	355	2	Q85308	Q85308 cowpox viru
45	224	10.3	349	2	O57098	O57098 camelpox vi

ALIGNMENTS

RESULT 1
T11B_MOUSE
ID T11B_MOUSE STANDARD; PRT; 401 AA.
AC O08712; O70202;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN Name=Tnfrsf1b; Synonyms=OCIF, OPG;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485; DOI=10.1016/S0092-8674(00)80209-3;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA DeRose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
AND ARG-296.
RC STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
RX MEDLINE=98382527; PubMed=9714833; DOI=10.1016/S0378-1119(98)00295-9;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA Higashio K.;
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
gene and its expression in embryogenesis.";
RL Gene 215:339-343(1998).
RN [3]
RP FUNCTION.
RX MEDLINE=21060987; PubMed=10952716;
RA Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
RA Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
RA Simonet W.S.;
RT "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
osteoclasts and prevents vascular calcification by blocking a process
resembling osteoclastogenesis.";
RL J. Exp. Med. 192:463-474(2000).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
its function in osteoclastogenesis. Inhibits the activation of
osteoclasts and promotes osteoclast apoptosis in vitro. Bone
homeostasis seems to depend on the local RANKL/OPG ratio. May also
play a role in preventing arterial calcification. May act as decoy
receptor for TRAIL and protect against apoptosis. TRAIL binding
blocks the inhibition of osteoclastogenesis.

CC -I- SUBUNIT: Homodimer.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
CC intestines and calvaria. Highly expressed in decidua and placenta,
CC and in embryo.
CC -I- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
CC whereas expression decreases at day 11 and increases from day 15
CC to 17. On day 15 found in developing bone primordia,
CC brachiocephalic artery and ductus arteriosus, left main bronchus,
CC abdominal aorta and midgut.
CC -I- INDUCTION: Up-regulated by TGF-beta and estrogens. Down-regulated
CC by 1,25-dihydroxyvitamin D3 and parathyroid hormone.
CC -I- SIMILARITY: Contains 2 death domains.
CC -I- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: U94331; AAB33708.1; -
CC EMBL: AB013898; BAA28269.1; -
CC EMBL: AB013903; BAA33388.1; -
CC EMBL: AB013899; BAA33388.1; JOINED.
CC EMBL: AB013900; BAA33388.1; JOINED.
CC EMBL: AB013901; BAA33388.1; JOINED.
CC EMBL: AB013902; BAA33388.1; JOINED.
CC HSSP: O14763; IDOG.
CC MGD; MGI:109587; Tnfrsf11b.
CC GO; GO:0005578; C:extracellular matrix; IDA.
CC InterPro: IPR000488; Death.
CC InterPro: IPR011029; DEATH like.
CC InterPro: IPR009030; Growth_fac_recept.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00020; TNFR_c6; 3.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS50017; DEATH DOMAIN; 1.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Apoptosis; Glycoprotein; Polymorphism; Receptor; Repeat; Signal.
CC SIGNAL 1 21 By similarity.
CC CHAIN 22 401 Tumor necrosis factor receptor
CC superfamily member 11b.
CC
CC REPEAT 24 62 TNFR-Cys 1.
CC REPEAT 65 105 TNFR-Cys 2.
CC REPEAT 107 142 TNFR-Cys 3.
CC REPEAT 145 185 TNFR-Cys 4.
CC REPEAT 198 269 Death 1.
CC DOMAIN 283 365 Death 2.
CC SITE 400 400 Involved in dimerization (By similarity).
CC
CC DISULFID 41 54 By similarity.
CC DISULFID 44 62 By similarity.
CC DISULFID 65 80 By similarity.
CC DISULFID 83 97 By similarity.
CC DISULFID 87 105 By similarity.
CC DISULFID 107 118 By similarity.
CC DISULFID 124 142 By similarity.
CC DISULFID 145 160 By similarity.
CC DISULFID 166 185 By similarity.
CC DISULFID 198 98 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 165 165 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 289 289 R -> P (in strain 129/Ola and strain NIH
CC VARIANT 138 138 Swiss).
CC
CC VARIANT 161 161 I -> R (in strain 129/Ola and strain NIH
CC VARIANT 165 165 N -> D (in strain 129/Ola and strain NIH
CC Swiss).

FT VARIANT 288 288 S -> A (in strain 129/Ola and strain NIH
FT Swiss).
FT VARIANT 296 296 L -> R (in strain 129/Ola and strain NIH
FT Swiss).
SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;
Query Match 100.0%; Score 2179; DB 1; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.8e-143;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNKWLCCALLVLLDIIIEWTQTETLPKYLHYDPETHGQLLCKCAPGTLYLKQHTVRRKT 60
DB 1 MNKWLCCALLVLLDIIIEWTQTETLPKYLHYDPETHGQLLCKCAPGTLYLKQHTVRRKT 60
QY 61 LCVPCPDHSYDTSWHTSDECVYCSVCKELOSQVCEKRNTHRVCECEGRVLETFECLK 120
DB 61 LCVPCPDHSYDTSWHTSDECVYCSVCKELOSQVCEKRNTHRVCECEGRVLETFECLK 120
QY 121 HRSCTPPGSGVQAGTPERNTVCKKCPDGFSSKAPCIKHTKNCSTFGLLLIQKGNAT 180
DB 121 HRSCTPPGSGVQAGTPERNTVCKKCPDGFSSKAPCIKHTKNCSTFGLLLIQKGNAT 180
QY 181 HDNVCSGNREATQKCGIDVTLCCEAFPRFAVPTKIIPNWLSDVSLPOTKVNASVERI 240
DB 181 HDNVCSGNREATQKCGIDVTLCCEAFPRFAVPTKIIPNWLSDVSLPOTKVNASVERI 240
QY 241 KRRHSSQSQTFOLLKWKHQRNDQEWVKKIQDIDLCSSVORHLGHSLNTTEQLLALME 300
DB 241 KRRHSSQSQTFOLLKWKHQRNDQEWVKKIQDIDLCSSVORHLGHSLNTTEQLLALME 300
QY 301 SLPGKKISPEEIERTRKTKSKSEQLKLLSLWRINKNGQDTLKGLMYALKHLKTSHPFKT 360
DB 301 SLPGKKISPEEIERTRKTKSKSEQLKLLSLWRINKNGQDTLKGLMYALKHLKTSHPFKT 360
QY 361 VTHSLRKTMRFLHSPTMYRLYOKLFLEMIGNOVQSVKISCL 401
DB 361 VTHSLRKTMRFLHSPTMYRLYOKLFLEMIGNOVQSVKISCL 401
RESULT 2
Q8P112 PRELIMINARY; PRT; 401 AA.
AC Q6P112
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 11b
DE (Osteoprotegerin).
GN Name=TNfrsf11b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL "cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RA Strauberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049782; A049782.1; -
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0042489; P:negative regulation of ontogenesis (sensu. . . ; IDA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 401 AA; 45965 MW; 7C708E52EB46BA0E CRC64;
Query Match 99.1%; Score 2159; DB 2; Length 401;
Best Local Similarity 99.0%; Pred. No. 4.5e-142;
Matches 397; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNKWLCCNLAVALDIETWTTQETLPKYLHYDPETGHLCDKCAPGTYLKQHCIVRRKT 60
DB 1 MNKWLCCNLAVALDIETWTTQETLPKYLHYDPETGHLCDKCAPGTYLKQHCIVRRKT 60
QY 61 LCVPCPDHSYTDWHTSDECVSPVKELQSVKQECNRTHNRVCEEGRYLEIFCLK 120
DB 61 LCVPCPDHSYTDWHTSDECVSPVKELQSVKQECNRTHNRVCEEGRYLEIFCLK 120
QY 121 HRSPPGSGVQAGTPERNTVCKKPDGFFSGTSSKAPCIKHTNCSTFGLLIQKGNAT 180
DB 121 HRSPPGSGVQAGTPEQNTVCKKPDGFFSGTSSKAPCRKHTNCSTFGLLIQKGNAT 180
QY 181 HDNVCSGNREATKCGIDVTLCHEAFRFAVPVKIIPNWLVLVDSLPGTKVAESVERI 240
DB 181 HDNVCSGNREATKCGIDVTLCHEAFRFAVPVKIIPNWLVLVDSLPGTKVAESVERI 240
QY 241 KRRHSSQEQTFQLLKWKHQRNDQEMVKIIQIDILCESSVQRHLGHSNLTTEQLALME 300
DB 241 KRRHSSQEQTFQLLKWKHQRNDQEMVKIIQIDILCESSVQRHLGHANLTTEQLALME 300
QY 301 SLPGKKISPEIERTRTKTCKSSQQLKLSLWRIKNGDQDTLKGMLYALKHKTSHPPKT 360
DB 301 SLPGKKISPEIERTRTKTCKSSQQLKLSLWRIKNGDQDTLKGMLYALKHKTSHPPKT 360
QY 361 VTHSLRKTWFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
DB 361 VTHSLRKTWFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
RESULT 3
TIIB_RAT STANDARD; PRT; 401 AA.
AC O08727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin).
GN Names=Tnfrsf11b; Synonyms=Opg;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestine;
RX MEDLINE=97262071; PubMed=9108485; DOI=10.1016/S0092-8674(00)80209-3;
RA Liemont W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RL of bone density";
RL Call 89:309-315(1997).
CC -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- INDUCTION: Up-regulated by osteopontin.
CC -1- SIMILARITY: Contains 2 death domains.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
CC or send an email to license@ebi.ac.uk).
CC EMBL; U94330; AAB53707.1; -
DR HSP; P19438; INCF.
DR RGD; 619802; Tnfrsf11b.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR009030; Growth factor receptor.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Apoptosis; Cytokine; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21 By similarity.
FT CHAIN 22 401 Tumor necrosis factor receptor
FT REPEAT 24 62 superfamily member 11B.
FT REPEAT 65 105 TNFR-Cys 1.
FT REPEAT 107 142 TNFR-Cys 2.
FT REPEAT 145 185 TNFR-Cys 3.
FT REPEAT 198 269 TNFR-Cys 4.
FT DOMAIN 270 365 Death 1.
FT SITE 400 400 Death 2.
FT SITE 401 400 Involved in dimerization (By similarity).
FT DISULFID 41 54 By similarity.
FT DISULFID 44 62 By similarity.
FT DISULFID 65 80 By similarity.
FT DISULFID 83 97 By similarity.
FT DISULFID 107 118 By similarity.
FT DISULFID 124 142 By similarity.
FT DISULFID 145 160 By similarity.
FT DISULFID 166 185 By similarity.
FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 165 165 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 289 289 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 401 AA; 46192 MW; F6C6A31F1D4E573A CRC64;
Query Match 95.4%; Score 2079; DB 1; Length 401;

Best Local Similarity 94.5%; Pred. No. 1.6e-136;

Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIETWTTQETLPKYLHYDPETGQHLCDKCAPTYLKHQCTVRRKT 60
DB 1 MNKWLCCALLVLLDIIETWTTQETFPKYLHYDPETGQHLCDKCAPTYLKHQCTVRRKT 60
QY 61 LCVPCPDHYSYDTSWHTSDCVYCSVKELQSVKQECNTRNVRVCEBGRYLEIFCLK 120
DB 61 LCVPCPDHYSYDTSWHTSDCVYCSVKELQSVKQECNTRNVRVCEBGRYLEIFCLK 120
QY 121 HRSPPGSGVQAGTERTNVTCKCPDGFSGTSSKAPCIKHTNCSTGILLIQGNAT 180
DB 121 HRSPPGSGVQAGTERTNVTCKCPDGFSGTSSKAPCIKHTNCSTGILLIQGNAT 180
QY 181 HDNVCSGNEATQCCGIDVTLCEAFRFAVPTKIIPNWLVLVSLPCTKNAESVERI 240
DB 181 HDNVCSGNEATQCCGIDVTLCEAFRFAVPTKIIPNWLVLVSLPCTKNAESVERI 240
QY 241 KRHSQEQTPQLLKLWKHQNDRDQEMVKKIIQDIDLCSSVQRHLGSHNLTTQQLALME 300
DB 241 KRHSQEQTPQLLKLWKHQNDRDQEMVKKIIQDIDLCSSVQRHLGSHNLTTQQLALME 300
QY 301 SLPGKISPEERTKTKCSQELLKLSLWRKNGDQDTLKLGMVYALKHLKTSHPKPT 360
DB 301 SLPGKISPEERTKTKCPSEQLLKLSLWRKNGDQDTLKLGMVYALKHLKTSHPKPT 360
QY 361 VTHSLRKTWRFLHSFTMYRLYOKLFLEMTGNQVQSVKISCL 401
DB 361 VTHSLRKTWRFLHSFTMYRLYOKLFLEMTGNQVQSVKISCL 401

RESULT 4

T11B HUMAN STANDARD; PRT; 401 AA.
AC 00030; 060236; Q9UHP4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
(Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN Names=TNFRSF11B; Synonyms=OCIF, OPG,
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485; DOI=10.1016/S0092-8674(00)80209-3;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung cancer;
RX MEDLINE=98151033; PubMed=9492069; DOI=10.1210/en.139.3.1329;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yanaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Placenta;

RE MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor";
RL Eur. J. Biochem. 254:685-691(1998).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS ASN-3 AND MET-104.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Peol C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;
RT "NIHNS-SNPs, environmental genome project, NIHNS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE=98238645; PubMed=9571159; DOI=10.1006/bbrc.1998.8443;
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.;
RT "Characterization of monomeric and homodimeric forms of
RT osteoclastogenesis inhibitory factor";
RL Biochem. Biophys. Res. Commun. 245:382-387(1998).
RN [7]
RP SEQUENCE OF 22-36.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Hensel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites";
RL Protein Sci. 13:2819-2824(2004).
RN [8]
RP SEQUENCE OF 22-393 FROM N.A.
RC TISSUE=Placenta;
RX PubMed=12110935;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and expression of osteoprotegerin from Homo sapiens";
RL Acta Biochim. Biophys. Sin. 31:680-684(1999).
RN [9]
RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION
RX MEDLINE=97312536; PubMed=9168977; DOI=10.1006/bbrc.1997.6503;
RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA Morinaga T., Higashio K.;
RT "Isolation of a novel cytokine from human fibroblasts that
RT specifically inhibits osteoclastogenesis";
RL Biochem. Biophys. Res. Commun. 234:137-142(1997).
RN [10]
RP TRAIL BINDING.
RX MEDLINE=98269100; PubMed=9603945; DOI=10.1074/jbc.273.23.14363;
RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,
RA James I.E., Rosenberg M., Lee J.C., Young P.R.;

"Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
[11]

CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
MEDLINE=98148058; PubMed=9478964; DOI=10.1074/jbc.273.9.5117;
Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
Moriwaga T., Higashio K.;
"Characterization of structural domains of human osteoclastogenesis
inhibitory factor.";
J. Biol. Chem. 273:5117-5123(1998).

[12]

REVIEW.
MEDLINE=21395914; PubMed=11505389;
DOI=10.1002/1097-0142(20010801)92:3<460::AID-CNCR1344>3.0.CO;2-D;
Hofbauer L.C., Neubauer A., Heufelder A.E.;
"Receptor activator of nuclear factor-kappaB ligand and
osteoprotegerin: potential implications for the pathogenesis and
treatment of malignant bone diseases.";
Cancer 92:460-470(2001).

[13]

VARIANT JPD ASP-182 DEL.
PubMed=12189164; DOI=10.1093/hmg/11.18.2119;
Cundy T., Hegde M., Naot D., Chong B., King A., Wallace R., Mulley J.,
Love D.R., Seidel J., Fawcett M., Banovic T., Callon K.E., Grey A.B.,
Reid I.R., Middleton-Hardie C.A., Cornish J.;
"A mutation in the gene TNFRSF11B encoding osteoprotegerin causes an
idiopathic hyperphosphatasia phenotype.";
Hum. Mol. Genet. 11:2119-2127(2002).

-I- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
its function in osteoclastogenesis. Inhibits the activation of
osteoclasts and promotes osteoclast apoptosis in vitro. Bone
homeostasis seems to depend on the local RANKL/OPG ratio. May also
play a role in preventing arterial calcification. May act as decoy
receptor for TRAIL and protect against apoptosis. TRAIL binding
blocks the inhibition of osteoclastogenesis.

-I- SUBUNIT: Homodimer.

-I- SUBCELLULAR LOCATION: Secreted.
-I- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
lymph node, trachea, adrenal gland, testis, and bone marrow.
Detected at very low levels in brain, placenta and skeletal
muscle. Highly expressed in fetal kidney, liver and lung.

-I- INDUCTION: Up-regulated by increasing calcium-concentration in the
medium and estrogens. Down-regulated by glucocorticoids.
-I- PTM: N-glycosylated. Contains sialic acid residues.

-I- PTM: The N-terminus is blocked.

-I- DISEASE: Defects in TNFRSF11B are the cause of juvenile Paget
disease (JPD) [MIM:239000]; also called hyperostosis corticalis
deformans juvenilis or hereditary hyperphosphatasia or chronic
congenital idiopathic hyperphosphatasia. JPD is a rare autosomal
recessive osteopathy that presents in infancy or early childhood.
The disorder is characterized by rapidly remodeling woven bone,
osteopenia, debilitating fractures, and deformities due to a
markedly accelerated rate of bone remodeling throughout the
skeleton. Approximately 40 cases of JPD have been reported
worldwide. Unless it is treated with drugs that block osteoclast-
mediated skeletal resorption, the disease can be fatal.

-I- SIMILARITY: Contains 2 death domains.

-I- SIMILARITY: Contains 4 TNFR-Cys repeats.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; U94332; AAB53709.1; -

EMBL; AB002146; BAA25910.1; -

EMBL; AB008822; BAA32076.1; -

EMBL; AB008821; BAA32076.1; JOINED.

EMBL; AY466112; AAR23265.1; -

EMBL; AY466112; AAR23265.1; -

DR EMBL; BC030155; AAH30155.1; -;
DR EMBL; AF134187; AAP20168.1; -;
DR HSSP; O14763; 1DOG.
DR Genew; HGNC:11909; TNFRSF11B.
DR H-InvDB; HIX0007748; -;
DR MIM; 603643; -;
DR MIM; 239000; -;
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0005125; F:cytokine activity; TAS.
DR GO; GO:0004872; P:receptor activity; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; Death-like.
DR InterPro; IPR009030; Growth_fac_recept.
DR InterPro; IPR009030; Growth_fac_recept.

Query Match 87.2%; Score 1900; DB 1; Length 401;
Best Local Similarity 85.8%; Pred. No. 4.6e-124;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLLDI-IEWTTQTPLPKYLHYDPETGHQLLCKCAPGTLYLKQHTVRRK 59
DB 1 MNKLLCCA-LVFLDISIKWTTQTPLPKYLHYDEETSHQLLCKDPPGTLYLKQHTAKWK 59
QY 60 TLCPGPDHSYDTSWHTSDECVYSPVKELQSKQECNRTHRVCECEGRYLEIEFCL 119
DB 60 TVCAPCPDHYTDSWHTSDECLYSPVKELQYVQECNRTHRVCECEGRYLEIEFCL 119
QY 120 KHRSCPPGSGVQAGTPERNVCKCPDGFPSGETSSKAPCIKHTNCSTFGLLIQKNA 179
DB 120 KHRSCPPGSGVQAGTPERNVCKCPDGFPSNETSKAPCRHTNCSTFGLLIQKNA 179
QY 180 THDNVCSGNREATKQKGDIVLCEEAFFPAVPTKIIPNWLSDLPLGCTKVNESVER 239
DB 180 THDNVCSGNREATKQKGDIVLCEEAFFPAVPTKIIPNWLSDLPLGCTKVNESVER 239
QY 240 IKRHSQSQTFOLLKWKHQRNDQEWKIIQDIDLCSSVORHLGHSNLTTEQLLALM 299
DB 240 IKRHSQSQTFOLLKWKHQRNDQEWKIIQDIDLCSSVORHLGHSNLTTEQLLALM 299
QY 300 ESUPGKGIKSPETERTKTKCSQELLKLLSLWRKNGDQDTLGLMYALKHKTSHFPK 359
DB 300 ESUPGKGIKSPETERTKTKCSQELLKLLSLWRKNGDQDTLGLMYALKHKTSHFPK 359
QY 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
DB 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 5
Q6GLN3 PRELIMINARY; PRT; 387 AA.
ID Q6GLN3
AC Q6GLN3
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE MGC84670 protein.
GN Name=MGC84670;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

CC -1- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
CC detected in adult stomach, spinal cord, lymph node, trachea,
CC spleen, colon and lung. Highly expressed in several primary tumors
CC from colon, stomach, rectum, esophagus and in SW480 colon
CC carcinoma cells.
CC
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; AF104419; AAD03056.1; -
CC ENBL; AF134240; AAD29688.1; -
CC ENBL; AF217796; AAF35244.1; -
CC ENBL; AF217793; AAF33685.1; -
CC ENBL; AF217794; AAF33686.1; -
CC ENBL; AY358279; AAQ88646.1; -
CC ENBL; AL121845; CAC03668.1; -
CC ENBL; BC017065; AAH17065.1; -
CC ENBL; BC034349; AAH34349.1; -
CC HSP; O14763; IDU3.
CC Genes; HGNC:11921; TNFRSF6B.
CC H-InVDB; HIX0016007; -
CC MIM; 603361; -
CC GO; GO:0005625; C:soluble fraction; TAS.
CC GO; GO:0004872; F:receptor activity; TAS.
CC GO; GO:0006916; P:anti-apoptosis; TAS.
CC InterPro; IPR009030; G:row fac_recept.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 4.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS00500; TNFR_NGFR_2; 2.
CC Apoptosis; Direct protein sequencing; Glycoprotein; Receptor; Repeat;
KW SIGNAL.
FT SIGNAL 1 29
FT CHAIN 30 300 Tumor necrosis factor receptor
FT
FT superfamily member 6B.
FT REPEAT 31 70
FT REPEAT 72 113 TNFR-Cys 1.
FT REPEAT 115 150 TNFR-Cys 2.
FT REPEAT 152 193 TNFR-Cys 3.
FT REPEAT 195 232 TNFR-Cys 4.
FT DISULFID 49 62 By similarity.
FT DISULFID 52 70 By similarity.
FT DISULFID 73 88 By similarity.
FT DISULFID 91 105 By similarity.
FT DISULFID 95 113 By similarity.
FT DISULFID 115 126 By similarity.
FT DISULFID 132 150 By similarity.
FT DISULFID 153 168 By similarity.
FT DISULFID 174 193 By similarity.
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;
Query Match 19.5%; Score 424.5; DB 1; Length 300;
Best Local Similarity 39.0%; Pred. No. 1.4e-21;
Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;
QY 26 PKLYHDPETGCHLLCDKCAPGYTLKQCHTVRRKTLVCPDHSYTDSDHSTDECVCSVC 85
DB 34 PTYPWRDAETGRVLCAQCPGPTVQRCRDRSPPTCGPCPRHVTQFWNYLCRYCNV 93
QY 86 VKELQSVKQECNRTNVRVCEEGRYLEIFCLKHSRCPGSGVQAGTPTERTVCKK 145
DB 94 LCGEERERARACHATHNRACRRTGFFAHAGFCLHSCPPGAGVIAFGTPTSQTCQCP 153
QY 146 PDGFFSGTSSKAPCIKHTNCTSTFGLLTIQKNATHDNV---CSGNREATORCKGIDVTL 202
DB 154 PGTFSASSSSSEQCPHNCNTALGLALNVPSSSHDLTCTGCTGFFPLSTRVPGAE--C 211

QY 203 EEAFFRFAVPTKIIPNWLVLVDSL 227
DB 212 ERAVIDFAVQDISIKRLQRLQAL 236
RESULT 9
Q6NW61 PRELIMINARY; PRT; 286 AA.
ID Q6NW61
AC Q6NW61
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE LOC407674 protein (Fragment).
GN Name=LOC407674;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067712; AAH67712.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF 2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
FT NON TER 1
SQ SEQUENCE 286 AA; 32275 MW; 9F43CDC5FAC4E77B CRC64;
Query Match 18.2%; Score 397.5; DB 2; Length 286;
Best Local Similarity 31.6%; Pred. No. 9.8e-20;
Matches 94; Conservative 44; Mismatches 118; Indels 41; Gaps 6;
QY 28 YLHYDPETGCHLLCDKCAPGYTLKQCHTVRRKTLVCPDHSYTDSDHSTDECVCSVC 87
DB 18 YRRKDPETGRTLECARCAPGSRRLQHCSSSRQTCSPGPGMGTFFWNYIPDCLLDCS-C 76
QY 88 KELOSQVQECNRTNVRVCEEGRYLEIFCLKHSRCPGSGVQAGTPTERTVCKKCPD 147
DB 77 AHRVVQPCNGIANTVCECEEGFYWQHFCRRHSVCRPGHGVKTAGTTPYSDTCEACAE 136

```

QY 148 GPFSGTSSKAPCIKHTNCTGFLLLIQKNATHDNCVSGNRATQKCGIDVTLCEAF 207
DB 137 GHFSDATKAQAQCVHRVQGEHLL--SGNTHYNSICTTCQQLSNGTWTVAFPDALS 195
QY 208 RPAVPTKIIPNWLVLVDSLPGTKVAESVERIKRRHSQEQFFQLLKLWKHQNRQDMV 267
DB 196 ALQVQKQIDIRLEQWV-----IRRLKK-----PLKQLHK----- 225
QY 268 KKIIDIDLCSSVQRHLGHSNITTTQLLALMSLPKPKISPEIRTRTKCKSSQ 324
DB 226 RTAMRRADPSEGLIDRSMLENSYLHQAQM-----TQNIIRVQSCNNIER 273

RESULT 10
Q9PUS0
ID Q9PUS0 PRELIMINARY; PRT; 302 AA.
AC Q9PUS0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20111091; PubMed=10642582;
RA Bobe J., Goetz F.W.;
RT "A tumor necrosis factor decoy receptor homologue is up-regulated in
RT the brook trout (Salvelinus fontinalis) ovary at the completion of
RT ovulation.";
RL Biol. Reprod. 62:420-426(2000).
DR EMBL; AF156738; AAD56428.1; -.
DR HSSP; O14763; 1D4V.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 17.9%; Score 390.5; DB 2; Length 302;
Best Local Similarity 42.7%; Pred. No. 3.2e-19;
Matches 67; Conservative 34; Mismatches 53; Indels 3; Gaps 2;

QY 32 DPETGQLLDCAPGTYLKQHTVVRKTLVCPDPHSYTDSDWHTSDVCYVCKELQ 91
DB 27 DRYSGLSIVCDRCPGTYLRAPCSAARKSDCACPGAYTEFWNHISKLRCS-MAENQ 85

QY 92 SVKQECNRTHNRVCEBGRYL--EIFCLKHSRCPGSGVVGQAGTPERNTVCKPDGF 149
DB 86 VVQECSPSNCECKEGYFNKYKVEACIKHKECPGICANTGTGPHQDTECVQCAQGF 145

QY 150 PSGETSKAPCIKHTNCTGFLLLIQKNATHDNCV 186
DB 146 YSEVSSAKATCLAQSNCKVGGLRVLKGQDMHNTLCA 182

RESULT 11
Q90W71
ID Q90W71 PRELIMINARY; PRT; 285 AA.
AC Q90W71;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative decoy receptor 3 protein.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Pleguezuelos O., Secombes C.J.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ315137; CAC43329.1; -.
DR HSSP; O14763; 1D0G.
DR GO; GO:0004872; F:receptor activity; IEA.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 285 AA; 31642 MW; FB75CFEC1B391AD0 CRC64;

Query Match 17.9%; Score 390; DB 2; Length 285;
Best Local Similarity 40.5%; Pred. No. 3.3e-19;
Matches 79; Conservative 25; Mismatches 81; Indels 10; Gaps 4;

QY 26 PKYLHYDPTGCHQLLDCAPGTYLKQHTVVRKTLVCPDPHSYTDSDWHTSDVCYV 85
DB 29 PTYINRDDATGDSLTCDLCAPGTYLKQHTVVRKTLVCPDPHSYTDSDWHTSDVCY 88

QY 86 VC--KELOSVKQECNRTHNRVCEBGRYLETEFLKHSRCPGSGVVGQAGTPERNTV 143
DB 89 FCTADEIESV--PCTQLHNRQCECKDGFYTHGSCSRHRRCPPGEGVINGTAHTDV 146

QY 144 KCPDGFSGTSSKAPCIKHTNCTGFLLLIQKNATHDNCV----GNREATQKCGIDV 199
DB 147 PCPVGFFSAVSSSRKACQKFSVCPGGTTI--PGNDMDNVYCSACTNGSRTHGEA 204

QY 200 TLCEAFAFPFAVPTK 214
DB 205 ELMEFLSLQLTPRK 219

RESULT 12
Q90YS6
ID Q90YS6 PRELIMINARY; PRT; 285 AA.
AC Q90YS6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE TNF decoy receptor.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21883732; PubMed=11886174; DOI=10.1006/cyto.2001.0979;
RA Liu L., Fujiki K., Dixon B., Sundick R.S.;
RT "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
RT with a fractalkine-like stalk and a TNF decoy receptor using cDNA
RT fragments containing AU-rich elements.";
RL Cytokine 17:71-81(2002).
DR EMBL; AF401631; AAK91758.1; -.
DR HSSP; O14763; 1D0G.
DR GO; GO:0004872; F:receptor activity; IEA.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 285 AA; 31795 MW; 5E3BD1B6EFC6BABC CRC64;

```

```
Query Match 17.6%; Score 383; DB 2; Length 285;
Best Local Similarity 41.0%; Pred. No. 1e-18;
Matches 80; Conservative 24; Mismatches 81; Indels 10; Gaps 5;

QY 26 PKYLHYDPETHGCHLLCDKCAPGYLKQHCTVRKTLVCPDHSYTDSTWHTSDVCYCSGP 85
DB 29 PTYIWRDDATGDSLTCDLCAAGPYLLKHCTKDRKSDGCPKSHYTEIWNRYCQYCNR 88
QY 86 VC--KELQSVKQECNTHNRVCECEBGRYLEIEFCLKHKRSCPPGSGVVOAGTPTERNVTK 143
DB 89 FCTADIESV--FCTQLHNRQCECKDGFYHTHSCSRHRRCPPGEGVINGTAHTDVKE 146
QY 144 KCPDGFSGTSSKAPCIKHTNGTSTFGLLIQKGNATHDNVCS---GNREATQKCGIDV 199
DB 147 PCFVGFFSAVSSSRKACQKFSVCPPT-GRIT- PGNDMNDVYCSACRNGSRTHGQAICDG 204
QY 200 TLCCEAFFRFAVPTK 214
DB 205 ELMEFLSLQLLTPTK 219

RESULT 13
Q62327
ID Q62327 PRELIMINARY; PRT; 459 AA.
AC Q62327;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumour necrosis factor receptor 2 protein (Fragment).
GN Name=TNFRsf1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor Necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice.";
RL Genomics 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=95178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -.
DR F01; I48854; I48854.
DR HSSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0018021; C:integral to membrane; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0008220; P:necrosis; IMP.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PSS0050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER
FT NON_TER
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 14.4%; Score 314; DB 2; Length 459;
Best Local Similarity 34.6%; Pred. No. 1.1e-13;
Matches 66; Conservative 20; Mismatches 79; Indels 26; Gaps 4;

QY 18 WTTQETLPPKYL--HYDPETHG-----QLLCDKCAPGYLKQHCTVRKTL 62
```

```
Db 2 WATCHTPVAQVVLTPYKPPGYECQISQBYDRKQACMCCAKCPGQYVHFNCNKTSDTVC 61
QY 63 VPCPDHSYTDSTWHTSDVCYCSVPVKELQSVKQECNTHNRVCECEBGRYLEIEF----- 117
Db 62 ADCEASMTYQVWNQFRITCLSSSSCSTQDVETRACTQQNRVCAACBAGRYCALKTHSGSC 121
QY 118 --CLHRSPPGSGVVOAGTPTERNVTKCPDGFSGTSSKAPCIKHTNCSTFGLLIQ 175
Db 122 RQCMRLSKGPGFGVASSRPAFNGVNLKACAPGTSTSSDVTDCNPHRICS-----ILAI 177
QY 176 KGNATHDNVCS 186
Db 178 PGNASTDAVCA 188

RESULT 14
TRIB HUMAN
ID TRIB HUMAN STANDARD; PRT; 461 AA.
AC P20333; Q16042; O6YI29; Q9UIH1;
DT 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Tumour necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (TNF-R2) (Tumor necrosis factor receptor
DE type II) (p75) (p80 TNF-alpha receptor) (CD120b) (Stanercept)
DE [Contains: Tumor necrosis factor binding protein 2 (TNFRI) (TBP-2)].
GN Name=TNFRSF1B; Synonyms=TNFR, TNFR2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90260639; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins.";
RL Science 248:1019-1023(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-196.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=96299745; PubMed=8661109; DOI=10.1006/geno.1996.0327;
RA Beltlinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA Brodeur G.M.;
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RL Genomics 35:94-100(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2), SUBCELLULAR LOCATION, AND FUNCTION OF
RP ISOFORM 2
RX PubMed=14688072; DOI=10.1093/intimm/dxh014;
RA Lainez B., Fernandez-Real J.M., Romero X., Esplugues E., Canete J.D.,
RA Ricart W., Engel P.;
RT "Identification and characterization of a novel spliced variant that
RT encodes human soluble tumor necrosis factor receptor 2.";
RL Int. Immunol. 16:169-177(2004).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS MET-187; ARG-196; LYS-232; THR-236;
RP PRO-264 AND ARG-295.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
```


RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND
 RP ARG-301.
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
 RA Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
 RA Nickerson D.A.;
 RA "SeattleSNPs: NHLBI HUG6682 program for genomic applications, UW-
 RT PHRCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=PNS;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Haieh F.,
 RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE OF 37-461 FROM N.A. (ISOFORM 1).
 RX MEDLINE=91370690; PubMed=1965549; DOI=10.1016/1043-4666(90)90022-I;
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
 RA Brockhaus M., Lesslauer W.;
 RT "Two human TNF receptors have similar extracellular, but distinct
 RT intracellular, domain sequences.";
 RL Cytokine 2:231-237(1990).
 RN [9]
 RP SEQUENCE OF 116-461 FROM N.A. (ISOFORM 1), PARTIAL SEQUENCE, AND
 RP VARIANT ARG-196.
 RX MEDLINE=90349572; PubMed=2166946;
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
 RA Ringold G.M.;
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor and
 RT demonstration of a shed form of the receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
 RN [10]
 RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
 RX MEDLINE=21069356; PubMed=11197692; DOI=10.1038/sj.gene.5363700;
 RA Teuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
 RT "New single nucleotide polymorphisms in the coding region of human
 RT TNFR2: association with systemic lupus erythematosus.";
 RL Genes Immun. 1:501-503(2000).
 RN [11]
 RP SEQUENCE OF 27-31.
 RC TISSUE=Urine;
 RX MEDLINE=90110215; PubMed=2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human urine.
 RT Evidence for immunological cross-reactivity with cell surface tumor
 RT necrosis factor receptors.";
 RL J. Biol. Chem. 265:1531-1536(1990).
 RN [12]
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE=91056048; PubMed=2173696;
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brockhaus M.;
 RT "Purification and partial amino acid sequence analysis of two distinct

RT tumor necrosis factor receptors from HL60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RN [13]
 RP CHARACTERIZATION.
 RX MEDLINE=93016040; PubMed=1328224;
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [14]
 RP INTERACTION WITH TRAF2.
 RX MEDLINE=94349371; PubMed=8059916; DOI=10.1016/0092-8674(94)90532-0;
 RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
 RT "A novel family of putative signal transducers associated with the
 RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
 RL Cell 78:681-692(1994).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ÅNGSTRÖMS) OF 419-428 IN COMPLEX WITH
 RP TRAF2.
 RX MEDLINE=99221490; PubMed=10206649; DOI=10.1038/19110;
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
 RT "Structural basis for self-association and receptor recognition of
 RT human TRAF2.";
 RL Nature 398:533-538(1999).
 RN [16]
 RP VARIANTS ARG-196 AND LYS-232.
 RX MEDLINE=21603988; PubMed=11762942;
 RA Morita C., Horiuchi T., Tsukamoto H., Hattori N., Kikuchi Y.,
 RA Arinobu Y., Otsuka T., Sawabe T., Harashina S., Nagasawa K., Niho Y.;
 RT "Association of tumor necrosis factor receptor type II polymorphism
 RT 196R with systemic lupus erythematosus in the Japanese: molecular and
 RT functional analysis.";
 RL Arthritis Rheum. 44:2819-2827(2001).
 RN [17]
 RP VARIANT ARG-196.
 RX MEDLINE=22151311; PubMed=12161545; DOI=10.1210/jc.87.8.3977;
 RA Peral B., San Millán J.L., Castello R., Moghetti P.,
 RA Escobar-Morreale H.F.;
 RT "Comment: the methionine 196 arginine polymorphism in exon 6 of the
 RT TNF receptor 2 gene (TNFRSF1B) is associated with the polycystic ovary
 RT syndrome and hyperandrogenism.";
 RL J. Clin. Endocrinol. Metab. 87:3977-3983(2002).
 CC -1- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
 CC approximately 5-fold lower affinity for homotrimeric
 CC TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the
 CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2. This
 CC receptor mediates most of the metabolic effects of TNF-alpha.
 CC Isoform 2 blocks TNF-alpha-induced apoptosis, which suggests that
 CC it regulates TNF-alpha function by antagonizing its biological
 CC activity.
 CC -1- SUBUNIT: Binds to TRAF2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
 CC secreted (isoform 2 and TRP-II).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P20333-1; Sequence=Displayed;
 CC Name=2; Synonyms=DS-TNFR2(Delta57,8), sTNFR2;
 CC IsoId=P20333-2; Sequence=VSP_011826, VSP_011827;
 CC -1- PTM: Phosphorylated; mainly on serine residues and with a very low
 CC level on threonine residues.
 CC -1- PTM: A soluble form (tumor necrosis factor binding protein 2) is
 CC produced from the membrane form by proteolytic processing.
 CC -1- PHARMACEUTICAL: Available under the name Enbrel (Immunex and
 CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid
 CC arthritis (RA). Enbrel consist of the extracellular ligand-binding
 CC portion of TNFRSF1B linked to an immunoglobulin Fc chain. It binds
 CC to TNF-alpha and blocks its interactions with receptors.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;

Db	6	LWVALPELOL--WATGHTVPAQVVLTPYKPEPGYECQISQYDYDRKAQMCCKPPEGQY	63
Qy	50	LKQHCTVRRKTLCPDHSYSDSHTSDECVYCPVKELQSVKQECNRTHNRVCEEE	109
Db	64	VKHFCKTSDTVCADCEASMYTQVWQFRTCLSCSSCTTDOVEIRACTKQONRVCAEA	123
Qy	110	GRYLEIEF-----CLKHRSPPGSGVQAGTPERNTVCKCPDPGPFSGETSSKAPCIK	162
Db	124	GRYCALKTHSGSCRCQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRP	183
Qy	163	HTWCSTFGLLLIOKGNATHDNVCS	186
Db	184	HRICS-----ILATPGNASTDAVCA	203

Search completed: March 8, 2005, 14:44:36
Job time : 80.1412 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:11 ; Search time 83.8966 Seconds
(without alignments)
1843.986 Million cell updates/sec

Title: US-09-389-782A-5
Perfect score: 2240
Sequence: 1 ETTPPKYLHYDEETSHQLLC.....VMHEALHNHYTQKLSLSLSPG 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2240	100.0	400	4	AAB80901 Human OPG
2	2240	100.0	400	4	AAY72919 Human OPG
3	2240	100.0	422	4	AAB66993 OPG-FC. 4
4	2227	99.4	406	4	AAB80902 Human OPG
5	2227	99.4	406	4	AAY72920 Human OPG
6	2225	99.3	425	5	ABG71831 Human OPG
7	2222.5	99.2	407	4	AAB80899 Human OPG
8	2222.5	99.2	407	4	AAY72917 Human ost
9	2218.5	99.0	413	4	AAB80900 Human OPG
10	2218.5	99.0	413	4	AAY72918 Human ost
11	2191	97.8	404	4	AAB80903
12	2191	97.8	404	4	AAY72921
13	1522.5	68.0	659	6	ABJ37103 Concatame
14	1522.5	68.0	659	8	ADQ79910 Human tum
15	1517	67.7	489	8	ADM32913 AMino aci
16	1514.5	67.6	490	6	ABJ37099 Concatame
17	1514.5	67.6	490	8	ADQ79902 Human tum
18	1514.5	67.6	720	6	ABJ37101 Concatame
19	1514.5	67.6	720	8	ADQ79906 Human tum
20	1502	67.1	518	4	AAB50080 TNFR:Fc F
21	1502	67.1	518	4	AAB70001 STNFR1075
22	1493	66.7	485	2	AAR24016 Fusion pr
23	1490.5	66.5	450	7	ADL06639 sTNFR1:1
24	1488	66.4	518	2	AAR51003 Sequence
25	1471.5	65.7	410	7	ADJ66000 Herpes vi

26	1471.5	65.7	440	8	ADP03589	Adp03589	Infection
27	1463	65.3	439	8	ADO47876	Ado47876	Alpha-Her
28	1461.5	65.2	443	6	ABP58181	Abp58181	Human RAN
29	1461.5	65.2	443	6	AAE34361	Aae34361	Human RAN
30	1459.5	65.2	444	5	ABG71833	Abg71833	RANK bind
31	1422.5	63.5	442	7	ADB17001	Adb17001	Human RAN
32	1422.5	63.5	443	7	ADB17002	Adb17002	Human RAN
33	1422	63.5	443	7	ADB17000	Adb17000	Murine RA
34	1392.5	62.2	608	6	ABJ37102	Abj37102	Concatame
35	1392.5	62.2	608	8	ADQ79908	Adq79908	Human tum
36	1384.5	61.8	444	6	ABJ37098	Abj37098	Concatame
37	1384.5	61.8	444	8	ADQ79900	Adq79900	Human tum
38	1384.5	61.8	628	6	ABJ37100	Abj37100	Concatame
39	1384.5	61.8	628	8	ADQ79904	Adq79904	Human tum
40	1352	60.4	376	2	AAW60037	Aaw60037	Antigenic
41	1350.5	60.3	396	8	ADP57557	Adp57557	Mouse ymk
42	1345.5	60.1	398	7	ABW02717	Abw02717	Mouse tms
43	1345.5	60.1	398	8	ADJ45758	Adj45758	Murine tm
44	1341.5	59.9	445	7	ADL06637	Adl06637	sTNFR1:1g
45	1337	59.7	376	2	AAW50287	Aaw50287	Human Fas

ALIGNMENTS

RESULT 1
AAB80901
ID AAB80901 standard; protein; 400 AA.
XX
AC AAB80901: 1 4
XX
DT 31-MAY-2001 (first entry)
XX
DE Human OPG(22-194)-FcdeltaC fusion protein.
XX
KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
KW osteoclast formation inhibition; bone resorption inhibition;
KW immunoglobulin.
XX
OS Homo sapiens.
XX
PN WO200117543-A2.
XX
PD 15-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-US022806.
XX
PR 03-SEP-1999; 99US-00389545.
XX
PA (AMGE-) AMGEN INC.
XX
PI Dunstan CR;
XX
DR WPI; 2001-265936/27.
XX
PT Preventing or treating lytic bone diseases, particularly associated with
PT cancer or metastasis, by administering an osteoprotegrin polypeptide.
XX
PS Claim 11; Fig 5; 87pp; English.

The present invention relates to a method for the prevention or treatment of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypeptide or OPG fusion protein. The present sequence is one such OPG fusion protein. OPG inhibits formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The OPG polypeptide can be used in a method of preventing or treating lytic bone disease, for preventing metastasis of cancer to bone (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophogeal, rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal tract, multiple myeloma or lymphoma) and preventing the osteosclerotic

CC bone metastasis. The OPG fusion polypeptides are used in the prevention
 CC or treatment of loss of bone mass, which occurs in conditions including
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
 CC congenital forms of osteoporosis (osteogenesis imperfecta,
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
 CC hyperthyroidism and renal function disorders; osteopaenia following
 CC surgery, induced by steroid administration, and associated with disorders
 CC of the small and large intestine and with chronic hepatic and renal
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
 CC are also used in the replacement of structurally sound bone with
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
 CC in adults and juveniles; hyperparathyroidism, in congenital bone
 CC disorders such as fibrous dysplasia, and in osteoclerotic bone
 CC metastases. The OPG fusion proteins can exhibit increased circulating
 CC half-lives and slower clearance times, thereby providing a more sustained
 CC activity. The OPG fusion protein comprises a fragment of the human OPG
 CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and
 CC CH3 regions; see AAB80897-8)

XX Sequence 400 AA;

Query Match 100.0%; Score 2240; DB 4; Length 400;
 Best Local Similarity 100.0%; Pred. No. 3e-130;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPPKYLHYDEETSHQLLCKDPCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 DB 1 ETFPPKYLHYDEETSHQLLCKDPCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVQAGTPERNTV 120
 DB 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVQAGTPERNTV 120
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQKVDKTHTC 180
 DB 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQKVDKTHTC 180
 QY 181 PPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPVRKFNWYVDGVEVHN 240
 DB 181 PPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPVRKFNWYVDGVEVHN 240
 QY 241 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 300
 DB 241 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 300
 QY 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFL 360
 DB 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFL 360
 QY 361 YSKLTVDKSRWQGNVFCFSVMHEALHNYHTQKSLSPG 400
 DB 361 YSKLTVDKSRWQGNVFCFSVMHEALHNYHTQKSLSPG 400

RESULT 2

AA72919

ID AAY72919 standard; protein; 400 AA.

XX

AC AAY72919;

XX

DT 13-JUN-2001 (first entry)

XX

DE Human OPG (22-194 aa)-Fc region (lacking 1-5 residues) fusion protein.

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
 KW periodontal.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .173
 FT /note= "Derived from human osteoprotegerin fragment (22-
 FT 194 residues)"
 FT Region 174
 FT /label= Linker
 FT Region 175. .400
 FT /note= Human IgG1 Fc region lacking 1-5 residues
 WO200118203-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-US022797.
 XX
 PR 03-SEP-1999; 99US-00389782.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Dunstan CR, Wooden SK, Mann MB;
 XX
 DR WPI; 2001-244572/25.
 XX
 PT Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
 PT by e.g. osteoporosis, Paget's disease and osteomyelitis.

XX Claim 7; Fig 5; 119pp; English.

XX The present sequence is a fusion protein comprising a sequence derived
 CC from human osteoprotegerin (OPG; 22-194 residues) which is fused with
 CC human immunoglobulin G1 (IgG1) Fc region lacking 1-5 residues by a
 CC linker. OPG negatively regulates the formation of osteoclasts in vitro
 CC and in vivo. It blocks the differentiation of osteoclasts from monocyte
 CC or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion
 CC protein is administered for the treatment of bone loss resulting from
 CC osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia
 CC associated with surgery or steroid administration, osteonecrosis, bone
 CC loss due to rheumatoid arthritis, periodontal bone loss, osteolytic
 CC metastasis and/or prosthetic loosening

XX Sequence 400 AA;

Query Match 100.0%; Score 2240; DB 4; Length 400;
 Best Local Similarity 100.0%; Pred. No. 3e-130;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPPKYLHYDEETSHQLLCKDPCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 DB 1 ETFPPKYLHYDEETSHQLLCKDPCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVQAGTPERNTV 120
 DB 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVQAGTPERNTV 120
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQKVDKTHTC 180
 DB 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQKVDKTHTC 180
 QY 181 PPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPVRKFNWYVDGVEVHN 240
 DB 181 PPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPVRKFNWYVDGVEVHN 240
 QY 241 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 300
 DB 241 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 300

Db 241 AKTKPREQNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGPREP 300
 Qy 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFL 360
 Db 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFL 360
 Qy 361 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 400
 Db 361 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 400

RESULT 3
 AAB66993
 ID AAB66993 standard; protein; 422 AA.
 AC AAB66993;
 XX
 XX
 DT 19-APR-2001 (first entry)
 XX
 DE OPG-Pc.
 KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
 KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
 KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
 KW ischaemia; Parkinson's disease.
 XX
 OS Unidentified.
 XX
 PN WO20103719-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 07-JUL-2000; 2000WO-US018667.
 XX
 PR 09-JUL-1999; 99US-00350670.
 PR 09-DEC-1999; 99US-00457647.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
 PI WPI; 2001-103031/11.
 DR N-PSDB; AAF57869.
 DR
 XX
 PT Treating conditions leading to bone loss such as rheumatoid arthritis,
 PT multiple sclerosis and asthma, comprises administering an osteoprotegerin
 PT protein in conjunction with e.g. inhibitors of interleukin and tumor
 PT necrosis factor alpha.
 XX
 PS Disclosure; Fig 29; 316pp; English.
 XX
 CC The present invention relates to a method for treating conditions leading
 CC to bone loss. The method comprises administering a purified and isolated
 CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)
 CC in conjunction with other substances such as tumour necrosis factor-alpha
 CC (TNF-alpha) inhibitors, interleukin (IL)-6 and -18 inhibitors, ICE
 CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet
 CC activating factor (PAF) antagonists. The method is useful for treating
 CC conditions leading to bone loss such as rheumatoid arthritis, multiple
 CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
 CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
 CC graft-versus-host disease (GVHD). Other diseases that can be treated
 CC include acute pancreatitis, Alzheimer's disease, anorexia,
 CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
 CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
 CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
 CC psoriasis and septic shock
 XX
 SQ Sequence 422 AA;

Query Match 100.0%; Score 2240; DB 4; Length 422;
 Best Local Similarity 100.0%; Fred. No. 3.2e-130; Indels 0; Gaps 0;
 Matches 400; Conservative 0; Mismatches 0;
 Qy 1 ETFFPKYLHYDETSQQLCDKCPGTYLKQHTAKWKTVCAPCPDHYTDSMHTSDECL 60
 Db 22 ETFFPKYLHYDETSQQLCDKCPGTYLKQHTAKWKTVCAPCPDHYTDSMHTSDECL 81
 Qy 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKXRSCTPPGFGVVQAGTPERTV 120
 Db 82 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKXRSCTPPGFGVVQAGTPERTV 141
 Qy 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKNATHDNICSGNSSTQKVDKTHTC 180
 Db 142 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKNATHDNICSGNSSTQKVDKTHTC 201
 Qy 181 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 240
 Db 202 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 261
 Qy 241 AKTKPREQNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGPREP 300
 Db 262 AKTKPREQNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGPREP 321
 Qy 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFL 360
 Db 322 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFL 381
 Qy 361 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 400
 Db 382 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 421

RESULT 4
 AAB80902
 ID AAB80902 standard; protein; 406 AA.
 XX
 AC AAB80902;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human OPG(22-201)-FcdeltaC fusion protein.
 XX
 KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
 KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
 KW osteoclast formation inhibition; bone resorption inhibition;
 KW immunoglobulin.
 XX
 OS Homo sapiens.
 XX
 PN WO200117543-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-US022806.
 XX
 PR 03-SEP-1999; 99US-00389545.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 XX Dunstan CR;
 PI WPI; 2001-265936/27.
 XX
 PT Preventing or treating lytic bone diseases, particularly associated with
 PT cancer or metastasis, by administering an osteoprotegrin polypeptide.
 XX
 PS Disclosure; Fig 6; 87pp; English.
 XX
 CC The present invention relates to a method for the prevention or treatment
 CC of lytic bone disease or multiple myeloma. Also the method can be used
 CC for preventing metastasis of cancer to bone or osteoclastic bone
 CC metastasis. The method comprises administering an OPG (osteoprotegrin)

CC polypeptide or OPG fusion protein. The present sequence is one such OPG
CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone
CC resorption) by blocking differentiation from monocytes/macrophage
CC precursors. The OPG polypeptide can be used in a method of preventing or
CC treating lytic bone disease, for preventing metastasis of cancer to bone
CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
CC rectal, bladder, cervical, ovarian, liver, and preventing the gastrointestinal
CC tract, multiple myeloma or lymphoma) and preventing the osteoclastic
CC bone metastasis. The OPG fusion polypeptides are used in the prevention
CC or treatment of loss of bone mass, which occurs in conditions including
CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
CC congenital forms of osteoporosis (osteogenesis imperfecta,
CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
CC due to immobilisation of extremities; Paget's disease of bone (osteitis
CC deformans) in adults and juveniles; osteomyelitis, or an infectious
CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
CC hyperthyroidism and renal function disorders; osteopaenia following
CC surgery, induced by steroid administration, and associated with disorders
CC of the small and large intestine and with chronic hepatic and renal
CC diseases; osteonecrosis, or bone cell death, associated with traumatic
CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
CC cell anaemia, systemic lupus erythematosus and other conditions; bone
CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
CC are also used in the replacement of structurally sound bone with
CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
CC in adults and juveniles; hyperparathyroidism, in congenital bone
CC disorders such as fibrous dysplasia, and in osteoclerotic bone
CC metastases. The OPG fusion proteins can exhibit increased circulating
CC half-lives and slower clearance times, thereby providing a more sustained
CC activity. The OPG fusion protein comprises a fragment of the human OPG
CC protein and the FC region of immunoglobulin IgGgamma1 (the hinge, CH2 and
CC CH3 regions; see AAB0897-8)
XX
SQ Sequence 406 AA;

Query Match 99.4%; Score 2227; DB 4; Length 406;
Best Local Similarity 98.5%; Pred. No. 2e-129;
Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
QY 1 ETFFPKYLHYDEETSHOLLCDKCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60
Db 1 ETFFPKYLHYDEETSHOLLCDKCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHKRSCPPGFGVVOAGTPERNTV 120
Db 61 YCSPVKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHKRSCPPGFGVVOAGTPERNTV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTKQGNATHDNCISGNSSESTQK-----V 174
Db 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTKQGNATHDNCISGNSSESTQKCGIDVTV 180
QY 175 DKHTHCPCCPAPELLGGPSVFLFPKPKDMLISTPTEVTCVVDVSHEDPVENKIVD 234
Db 181 DKHTHCPCCPAPELLGGPSVFLFPKPKDMLISTPTEVTCVVDVSHEDPVENKIVD 240
QY 235 GVEVHNATKPREQVNSTYRVVSVLTVLHQLNGKEYCKVSNKALPAPEKTIISKAK 294
Db 241 GVEVHNATKPREQVNSTYRVVSVLTVLHQLNGKEYCKVSNKALPAPEKTIISKAK 300
QY 295 GQPREFQVYTLPPSDELTCKNQSITCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 354
Db 301 GQPREFQVYTLPPSDELTCKNQSITCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 360
QY 355 DGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPG 400
Db 361 DGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPG 406

AAV72920
ID AAV72920 standard; protein; 406 AA.
XX
AC AAV72920;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human OPG (22-201 aa)-Fc region (lacking 1-5 residues) fusion protein.
XX
KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
KW periodontal.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..179
FT /note= "Derived from human osteoprotegerin fragment (22-
FT 201 residues)"
FT Region 180
FT /label= Linker
FT Region 181..406
FT /note= Human IgG1 Fc region lacking 1-5 residues;
FT (Corresponds to 6-231 residues of IgG1 Fc region)
XX
PN WO200118203-A1.
XX
PD 15-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-US022797.
XX
PR 03-SEP-1999; 99US-00389782.
XX
PA (AMGE-) AMGEN INC.
XX
PI Dunstan CR, Wooden SK, Mann MB;
XX
DR WPI; 2001-244572/25.
XX
PT Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
PT by e.g. osteoporosis, Paget's disease and osteomyelitis.
XX
PS Claim 7; Fig 6; 119pp; English.
XX
CC The present sequence is a fusion protein comprising a sequence derived
CC from human osteoprotegerin (OPG; 22-201 residues) which is fused with
CC human immunoglobulin G1 (IgG1) Fc region lacking 1-5 residues, by a
CC linker. OPG negatively regulates the formation of osteoclasts in vitro
CC and in vivo. It blocks the differentiation of osteoclasts from monocyte
CC or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion
CC protein is administered for the treatment of bone loss resulting from
CC osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia
CC associated with surgery or steroid administration, osteonecrosis, bone
CC loss due to rheumatoid arthritis, periodontal bone loss, osteolytic
CC metastasis and/or prosthetic loosening
XX
SQ Sequence 406 AA;

Query Match 99.4%; Score 2227; DB 4; Length 406;
Best Local Similarity 98.5%; Pred. No. 2e-129;
Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
QY 1 ETFFPKYLHYDEETSHOLLCDKCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60
Db 1 ETFFPKYLHYDEETSHOLLCDKCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHKRSCPPGFGVVOAGTPERNTV 120
Db 61 YCSPVKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHKRSCPPGFGVVOAGTPERNTV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTKQGNATHDNCISGNSSESTQK-----V 174

Db 121 CKKCPDGFPSNETSSKAPCKKHTNCSVFGLLLTQGNATHDNIICSGNSSTQKCGIDVTV 180
Qy 175 DKHTTCCPCAPAPELLGSPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 234
Db 181 DKHTTCCPCAPAPELLGSPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
Qy 235 GVEVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 294
Db 241 GVEVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
Qy 295 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 354
Db 301 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360
Qy 355 DGSFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNYTKQSLSPG 400
Db 361 DGSFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNYTKQSLSPG 406

RESULT 6
ABG71831
ID ABG71831 standard; protein; 425 AA.
AC ABG71831;
XX
XX
DT 14-APR-2003 (first entry)
XX
DE Human OPG protein for expression in mammalian cells.
XX
XX RANKL; human receptor activator of NFkappaB; osteoprotegerin; OPG;
KW RANK ligand; osteoclastogenesis; osteoclast inhibitor; gene therapy;
KW osteoporosis; bone disease; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200264782-A2.
PN
PD 22-AUG-2002.
XX
XX 08-FEB-2002; 2002WO-DK000090.
XX
XX 09-FEB-2001; 2001DK-00000214.
PR 09-FEB-2001; 2001US-0267843P.
PR 23-MAR-2001; 2001DK-00000498.
PR 23-MAR-2001; 2001US-0278320P.
XX
XX (MAXY-) MAXYGEN HOLDINGS LTD.
PA
XX
XX Haaning JM, Halkier T;
PI
XX
XX WPI: 2002-691592/74.
DR N-PSDB; ABS56347.
DR
XX
PT Novel human receptor activator of NFkappaB (hRANK) or human
PT osteoprotegerin (hOPG) variant polypeptides which bind to RANK ligand
PT (RANKL) with equivalent binding affinity as hRANK or hOPG, useful for
PT treating osteoporosis.
XX
XX Example 4; Fig 12; 129pp; English.
PS
XX This invention relates to a novel polypeptide having an amino acid
CC sequence that is different from and is at least about 70% identical to
CC the amino acid sequence of human receptor activator of NFkappaB (hRANK)
CC or human osteoprotegerin (hOPG), and which has a binding affinity to RANK
CC ligand (RANKL) that is at least as high as the binding affinity of hRANK
CC or hOPG to RANKL, as determined by functional competition assay. The
CC protein of the invention may have osteopathic activity and may act as a
CC RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclast activity
CC inhibitor. The nucleotide sequence shown in the invention may be used in
CC gene therapy. The protein of the invention or fusion proteins comprising a
CC this protein are useful as a pharmaceutical, and in the preparation of a

CC medicament for treating or preventing osteoporosis, or other bone
CC diseases or diseases associated with binding of RANKL to the RANK
CC receptor. A host cell containing a vector expressing the protein is
CC useful for producing a polypeptide having binding affinity to RANKL,
CC where the polypeptide comprises at least one N- or O-glycosylation site
CC and the host cell is a eukaryotic host cell capable of in vivo
CC glycosylation, and/or the polypeptide is subjected to conjugation to a
CC non-polypeptide moiety in vitro. The protein of the invention has
CC increased functional in vivo half-life and/or serum half-life compared to
CC hRANK or hOPG and has an improved binding affinity to RANKL compared to
CC the binding affinity of hRANK or hOPG to RANKL, as determined by a
CC functional competition assay. The present sequence represents a human OPG
CC protein modified for expression in a mammalian system; this sequence has
CC the human OPG protein fused to a leu-Glu dipeptide and amino acid
CC residues 247-475 of human IgG1
XX
XX Sequence 425 AA;
SQ
Query Match 99.3%; Score 2225; DB 5; Length 425;
Best Local Similarity 98.8%; Pred. No. 2.7e-129;
Matches 399; Conservative 1; Mismatches 0; Indels 4; Gaps 1;
Qy 1 ETTPPKYLHYDEETSHQLLCKDKCPGTYLKQHTAKWTVCAPCPDHYTDSMHTSDECL 60
Db 22 ETTPPKYLHYDEETSHQLLCKDKCPGTYLKQHTAKWTVCAPCPDHYTDSMHTSDECL 81
Qy 61 YCSPVKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERTV 120
Db 82 YCSPVKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERTV 141
Qy 121 CKRCPDGFPSNETSSKAPCKKHTNCSVFGLLLTQGNATHDNIICSGNSSTQKV---DK 176
Db 142 CKRCPDGFPSNETSSKAPCKKHTNCSVFGLLLTQGNATHDNIICSGNSSTQKLEKSSDK 201
Qy 177 THTCPCAPAPELLGSPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 236
Db 202 THTCPCAPAPELLGSPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 261
Qy 237 EVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 296
Db 262 EVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 321
Qy 297 PREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 356
Db 322 PREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 381
Qy 357 SFFLYSLKLTVDKSRWQOGNVFSCSVMHAEALHNYTKQSLSPG 400
Db 382 SFFLYSLKLTVDKSRWQOGNVFSCSVMHAEALHNYTKQSLSPG 425
RESULT 7
AAB80899
ID AAB80899 standard; protein; 407 AA.
XX
AC AAB80899;
XX
DT 31-MAY-2001 (first entry)
XX
XX Human OPG(22-194)-Fc fusion protein.
DE
XX
KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegerin;
KW osteoclast formation inhibition; bone resorption inhibition;
KW immunoglobulin.
XX
OS Homo sapiens.
XX
XX WO200117543-A2.
PN
XX
PD 15-MAR-2001.
XX
XX 18-AUG-2000; 2000WO-US022806.

XX 03-SEP-1999; 99US-00389545.
 XX (AMGE-) AMGEN INC.
 XX Dunstan CR;
 XX WPI; 2001-265936/27.
 XX Preventing or treating lytic bone diseases, particularly associated with
 XX cancer or metastasis, by administering an osteoprotegerin polypeptide.
 XX Disclosure; Fig 3; 87pp; English.
 XX The present invention relates to a method for the prevention or treatment
 XX of lytic bone disease or multiple myeloma. Also the method can be used
 XX for preventing metastasis of cancer to bone or osteoclastic bone
 XX metastasis. The method comprises administering an OPG (osteoprotegerin)
 XX polypeptide or OPG fusion protein. The present sequence is one such OPG
 XX fusion protein. OPG inhibits formation of osteoclasts (and thus bone
 XX resorption) by blocking differentiation from monocytes/macrophage
 XX precursors. The OPG polypeptide can be used in a method of preventing or
 XX treating lytic bone disease, for preventing metastasis of cancer to bone
 XX (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
 XX rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
 XX tract, multiple myeloma or lymphoma) and preventing the osteoclastic
 XX bone metastasis. The OPG fusion polypeptides are used in the prevention
 XX or treatment of loss of bone mass, which occurs in conditions including
 XX osteoporosis, such as primary osteoporosis, endocrine osteoporosis
 XX (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
 XX congenital forms of osteoporosis (osteogenesis imperfecta,
 XX homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
 XX due to immobilisation of extremities; Paget's disease of bone (osteitis
 XX deformans) in adults and juveniles; osteomyelitis, or an infectious
 XX lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
 XX and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
 XX leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
 XX hyperthyroidism and renal function disorders; osteopaenia following
 XX surgery, induced by steroid administration, and associated with disorders
 XX of the small and large intestine and with chronic hepatic and renal
 XX diseases; osteonecrosis, or bone cell death, associated with traumatic
 XX injury or nontraumatic necrosis associated with Gaucher's disease, sickle
 XX cell anaemia, systemic lupus erythematosus and other conditions; bone
 XX loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
 XX prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
 XX are also used in the replacement of structurally sound bone with
 XX disorganised bone as seen in Paget's disease of bone (osteitis deformans)
 XX in adults and juveniles; hyperparathyroidism, in congenital bone
 XX disorders such as fibrous dysplasia, and in osteoclastic bone
 XX metastases. The OPG fusion proteins can exhibit increased circulating
 XX half-lives and slower clearance times, thereby providing a more sustained
 XX activity. The OPG fusion protein comprises a fragment of the human OPG
 XX protein and the FC region of immunoglobulin IgGgamma1 (the hinge, CH2 and
 XX CH3 regions; see AAB80897-8)
 XX Sequence 407 AA;

Query Match 99.2%; Score 2222.5; DB 4; Length 407;
 Best Local Similarity 98.0%; Pred. No. 3,7e-129;
 Matches 399; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 ETPPKYLYHDETHSHQLCDKCPGTYLKQCTAKWTKVCAPCDPHYDTSWHTSDECL 60
 DB 1 ETPPKYLYHDETHSHQLCDKCPGTYLKQCTAKWTKVCAPCDPHYDTSWHTSDECL 60
 QY 61 YCSPVKELQYVKQCNTHNRVCSCKEGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120
 DB 61 YCSPVKELQYVKQCNTHNRVCSCKEGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120
 QY 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLTQKGNATHDNCISGNSSESTQKV----- 174
 DB 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLTQKGNATHDNCISGNSSESTQKAAEPKS 180

QY 175 -DKTHTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYV 233
 DB 181 CDKTHTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYV 240
 QY 234 DGVFVHNATKPRERQYNSYTRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKA 293
 DB 241 DGVFVHNATKPRERQYNSYTRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKA 300
 QY 294 KQOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 353
 DB 301 KQOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
 QY 354 SDGSFFLYSLKLTVDKSRMQQGNVFSCVVMHEALHNHYTQKSLSLSPG 400
 DB 361 SDGSFFLYSLKLTVDKSRMQQGNVFSCVVMHEALHNHYTQKSLSLSPG 407
 RESULT 8
 AAY72917
 ID AAY72917 standard; protein; 407 AA.
 XX AC AAY72917;
 XX DT 13-JUN-2001. (first entry)
 XX Human osteoprotegerin (22-194 residues)-IgG1 Fc region fusion protein.
 XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
 XX therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
 XX hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
 XX osteolytic metastasis; prostatic loosening; immunoglobulin G1; IgG1;
 XX periodontal.
 XX OS Homo sapiens.
 XX FH Key
 FT Region 1. .173
 FT /note= "Derived from human osteoprotegerin fragment (22-
 FT 194 residues)"
 FT Region 174. .176
 FT /label= Linker
 FT Region 177. .407
 FT /label= Human_IgG1_Fc_region
 WO200118203-A1.
 PD 15-MAR-2001.
 PF 18-AUG-2000; 2000WO-US022797.
 PR 03-SEP-1999; 99US-00389782.
 PA (AMGE-) AMGEN INC.
 XX Dunstan CR, Wooden SK, Mann MB;
 DR WPI; 2001-244572/25.
 XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
 XX by e.g. osteoporosis, Paget's disease and osteomyelitis.
 PS Example 1; Fig 3; 119pp; English.
 XX The present sequence is a fusion protein comprising a sequence derived
 XX from human osteoprotegerin (OPG; 22-194 residues) which is fused with
 XX human immunoglobulin G1 (IgG1) Fc region by a linker. OPG negatively
 XX regulates the formation of osteoclasts in vitro and in vivo. It blocks
 XX the differentiation of osteoclasts from monocyte or macrophage precursors
 XX and the reabsorption of bone. The OPG-Fc fusion protein is administered
 XX for the treatment of bone loss resulting from osteoporosis, Paget's
 XX disease, osteomyelitis, hypercalcaemia, osteopenia associated with
 XX surgery or steroid administration, osteonecrosis, bone loss due to
 XX rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or

CC prosthetic loosening
 XX
 SQ Sequence 407 AA;

Query Match 99.2%; Score 2222.5; DB 4; Length 407;
 Best Local Similarity 98.0%; Pred. No. 3.7e-129;
 Matches 399; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 ETFPKYLHYDETSQLLCDKCPGTYLKQHCTAKWTKVACPCPDHYTDSWHTSDCL 60
 |||||
 DB 1 ETFPKYLHYDETSQLLCDKCPGTYLKQHCTAKWTKVACPCPDHYTDSWHTSDCL 60
 |||||

QY 61 YCSPVKELQYVKECNTHNRVCEKGRYLEIEFCLKHSRCPGFGVQAGTPERNV 120
 |||||
 DB 61 YCSPVKELQYVKECNTHNRVCEKGRYLEIEFCLKHSRCPGFGVQAGTPERNV 120
 |||||

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKV----- 174
 |||||
 DB 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKAAAPKS 180
 |||||

QY 175 -DKTHTCPCPAPELLGGPSVFLPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWY 233
 |||||
 DB 181 CDKHTCPCPAPELLGGPSVFLPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWY 240
 |||||

QY 234 DGEVHNATKPREQYNSTYRVSVLTVLHODWLNGKEYCKVSNKALPAPIETISKA 293
 |||||
 DB 241 DGEVHNATKPREQYNSTYRVSVLTVLHODWLNGKEYCKVSNKALPAPIETISKA 300
 |||||

QY 294 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLD 353
 |||||
 DB 301 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLD 360
 |||||

QY 354 SDGSFELYSLKTVDKSRWQGNVFCVSNVHEALHNNHYTKSLSLSPG 400
 |||||
 DB 361 SDGSFELYSLKTVDKSRWQGNVFCVSNVHEALHNNHYTKSLSLSPG 407
 |||||

RESULT 9
 AAB80900
 ID AAB80900 standard; protein; 413 AA.
 AC AAB80900;
 XX
 XX 31-MAY-2001 (first entry)
 DE Human OPG(22-201)-Fc fusion protein.
 XX
 XX Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
 KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
 KW osteoclast formation inhibition; bone resorption inhibition;
 XX immunoglobulin.
 OS Homo sapiens.
 XX
 XX WO200117543-A2.
 XX
 XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-US022806.
 PF
 XX 03-SBP-1999; 99US-00389545.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Dunstan CR;
 FI
 XX WPI; 2001-265936/27.
 XX
 XX Preventing or treating lytic bone diseases, particularly associated with
 PT cancer or metastasis, by administering an osteoprotegrin polypeptide.
 XX Disclosure; Fig 4; 87pp; English.
 XX

Dd 361 TTPVLDSGDFLYSKLTVDKSRWQGNVFSCSNMHEALHNNHYTKLSLSLSPG 413

RESULT 10
AAV72918

ID	AAV72918 standard; protein; 413 AA.
XX AC	AAY72918;
XX DT	13-JUN-2001 (first entry)
DE DE	Human osteoprotegerin (22-201 residues)-IgG1 Fc region fusion protein.
XX KW	Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic; therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis; hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis; osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1; periodontal.
OS OS	Homo sapiens.
XX FT	Key Location/Qualifiers
FF Region	1..179 /note= "Derived from human osteoprotegerin fragment (22-
FT FT	201 residues) "
FT Region	180..182 /label= Linker
FT FT	Region 183..413 /label= Human_IgG1_Fc_region
XX FN	WO200118203-A1.
PX PD	15-MAR-2001.
XX PF	18-AUG-2000; 2000WO-USO22797.
PR PR	03-SEP-1999; 99US-00389782. (AMGE-) AMGEN INC.
PA PI	Dunstan CR, Wooden SK, Mann MB;
DR DR	WPI; 2001-244572/25.
PT PT	Osteoprotegerin-Fc protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis.
PS PS	Example 1; Fig 4; 119pp; English.
CC CC	The present sequence is a fusion protein comprising a sequence derived from human osteoprotegerin (OPG; 22-201 residues) which is fused with human immunoglobulin G1 (IgG1) Fc region by a linker. OPG negatively regulates the formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or macrophage precursors and the absorption of bone. The OPG-Fc fusion protein is administered for the treatment of bone loss resulting from osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia associated with surgery or steroid administration, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic loosening
SQ SQ	Sequence 413 AA;

Query Match	99.0%; Score 2218.5; DB 4; Length 413;
Best Local Similarity	96.6%; Pred. No. 6.7e-129;
Matches 399; Conservative	0; Mismatches 1; Indels 13; Gaps 1

QY 1 ETTFPKYLHYDEETSHQLCDKCPGGTYLKQHCTAKWKTCAPCRHYTSDSWHTSDECL 60
| | | | |
Db 1 ETTFPKYLHYDEETSHQLCDKCPGGTYLKQHCTAKWKTCAPCRHYTSDSWHTSDECL 60
| | | | |
QY 61 YCSFVKELQYKBECNTHNRVCCEGRGYLETFCLKHRSPPGPFGVVQAQTPERNTV 120
| | | | |

CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
 CC congenital forms of osteoporosis (osteogenesis imperfecta,
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
 CC hyperthyroidism and renal function disorders; osteopaenia following
 CC surgery, induced by steroid administration, and associated with disorders
 CC of the small and large intestine and with chronic hepatic and renal
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
 CC are also used in the replacement of structurally sound bone with
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
 CC in adults and juveniles; hyperparathyroidism, in congenital bone
 CC disorders such as fibrous dysplasia, and in osteoclerotic bone
 CC metastases. The OPG fusion proteins can exhibit increased circulating
 CC half-lives and slower clearance times, thereby providing a more sustained
 CC activity. The OPG fusion protein comprises a fragment of the human OPG
 CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and
 CC CH3 regions; see AAB80897-8)

XX
 SQ Sequence 404 AA;

Query Match 97.8%; Score 2191; DB 4; Length 404;
 Best Local Similarity 97.8%; Pred. No. 3.2e-127;
 Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;
 QY 1 ETFPPKYLHYDETSHQLLCDKCPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60
 Db 1 ETFPPKYLHYDETSHQLLCDKCPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTTPERTV 120
 Db 61 YCSPVKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTTPERTV 120
 QY 121 CKRCPDGFSENETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKV---DK 176
 Db 121 CKRCPDGFSENETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKV---DK 176
 QY 177 THTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 236
 Db 181 GGTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 240
 QY 237 EVHNAKTPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 296
 Db 241 EVHNAKTPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 300
 QY 297 PREPQVYTLPPSDELTKQVSLTCLVKGYFSDIAVEWESNGQPENNYKTPPVLDSDG 356
 Db 301 PREPQVYTLPPSDELTKQVSLTCLVKGYFSDIAVEWESNGQPENNYKTPPVLDSDG 360
 QY 357 SFPLYSKLTVDKSRWQGNVFCVSMHEALHNYTKQSLSLSPG 400
 Db 361 SFPLYSKLTVDKSRWQGNVFCVSMHEALHNYTKQSLSLSPG 404

RESULT 12
 AAY72921

ID AAY72921 standard; protein; 404 AA.

XX AAY72921;

XX 13-JUN-2001 (first entry)

DE Human OPG (22-194 residues)-FCG10 fusion protein.

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
 XX periodontal.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .173
 FT /note= "Derived from human osteoprotegerin fragment (22-
 FT 194 residues)"
 FT Region 174. .182
 FT /label= Ser-(Gly)8 linker
 FT Region 183. .404
 FT /note= Corresponds to 10-231 residues of human IgG1 Fc
 FT region
 PN WO200118203-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-US022797.
 XX
 PR 03-SEP-1999; 99US-00389782.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Dunstan CR, Wooden SK, Mann MB;
 XX WPI; 2001-244572/25.
 DR
 XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
 FT by e.g. osteoporosis, Paget's disease and osteomyelitis.
 FT
 XX Claim 7; Fig 7; 119pp; English.
 XX
 CC The present sequence is a fusion protein comprising a sequence derived
 CC from human osteoprotegerin (OPG; 22-194 residues) which is fused with
 CC human immunoglobulin G1 (IgG1) FcG10 region (lacks 1-9 residues and has a
 CC Ser-(Gly)8 linker). OPG negatively regulates the formation of osteoclasts
 CC in vitro and in vivo. It blocks the differentiation of osteoclasts from
 CC monocyte or macrophage precursors and the reabsorption of bone. The OPG-
 CC Fc fusion protein is administered for the treatment of bone loss
 CC resulting from osteoporosis, Paget's disease, osteomyelitis,
 CC hypercalcaemia, osteopenia associated with surgery or steroid
 CC administration, osteonecrosis, bone loss due to rheumatoid arthritis,
 CC periodontal bone loss, osteolytic metastasis and/or prosthetic loosening
 XX Sequence 404 AA;

Query Match 97.8%; Score 2191; DB 4; Length 404;
 Best Local Similarity 97.8%; Pred. No. 3.2e-127;
 Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;
 QY 1 ETFPPKYLHYDETSHQLLCDKCPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60
 Db 1 ETFPPKYLHYDETSHQLLCDKCPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTTPERTV 120
 Db 61 YCSPVKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTTPERTV 120
 QY 121 CKRCPDGFSENETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKV---DK 176
 Db 121 CKRCPDGFSENETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKV---DK 176
 QY 177 THTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 236
 Db 181 GGTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 240
 QY 237 EVHNAKTPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 296
 Db 241 EVHNAKTPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 300

QY 297 PREPQVTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG 356
DB 301 PREPQVTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG 360
QY 357 SFELYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPG 400
DB 361 SFELYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPG 404
RESULT 13
ID ABJ37103 standard; protein; 659 AA.
AC ABJ37103;
XX
XX
DT 08-MAY-2003 (first entry)
XX
DE Concatameric immunoadhesion human protein sequence SEQ ID No 12.
XX
XX Antinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW dimeric protein; inflammation; septicemia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation; human.
XX
XX Homo sapiens.
OS
XX WO2003010202-A1.
XX
XX
PD 06-FEB-2003.
XX
XX
PF 26-JUL-2002; 2002WO-KR001427.
XX
XX 26-JUL-2001; 2001KR-00045028.
XX
XX (WEDE-) MEDEXGEN CO LTD.
XX
XX
PI Chung Y, Han J, Lee H, Choi E, Kim J;
XX
XX WPI; 2003-229639/22.
DR N-PSDB; ABT32046.
XX
XX
PT New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.
XX
XX Claim 27; Page 148-152; 211pp; English.
XX
XX
CC The invention relates to a novel concatameric protein comprising two
CC soluble domains, in which an N-terminus of a soluble domain of a
CC biologically active protein is linked to a C-terminus of an identical
CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC related diseases. This sequence represents the human concatameric protein
CC of the invention
XX
SQ Sequence 659 AA;
Query Match 68.0%; Score 1522.5; DB 6; Length 659;
Best Local Similarity 65.4%; Pred. No. 1e-85;
Matches 295; Conservative 16; Mismatches 75; Indels 65; Gaps 5;
QY 9 HYDETSHOLLCDKCPGTYLKQHTAKWTKVCAPCPDHYHYTDSWHTSDECLYCSPVCKE 68
DB 214 YFDQ--TAQMCCSKSPGQHAQVCTKTSVTDVCDSCEDSTYQLWNWVPECLSCGRCS 271
QY 69 LQYVQECNRNTHRVCECKEGRYLEI-----EFLCKHRSPPGFGVQAGTPERTVCKE 122
DB 272 DQVETQACTREQNRCTCRPGWYCALSKQEGCLCAPLRCRPGFGVARGPTETSDVCK 331

QY 123 RCPDGFSSNETSSKAPCRKHTNCSVFLLLTQKGNATHDNIC----- 164
DB 332 PCAPGTFSNTSTSDICRPHQICNVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 387
QY 165 --SGNSESTQ-----KVDKTHTCPPCPAPELL 189
DB 388 PVSTRSQHTPTPEPSTAPSTSFLLPMGPPSPAEGSTGDAEPKSCDKTHTCPPCPAPELL 447
QY 190 GGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQ 249
DB 448 GGPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQ 507
QY 250 YNSTYRVVSVLTVLHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 309
DB 508 YNSTYRVVSVLTVLHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 567
QY 310 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKS 369
DB 568 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKS 627
QY 370 RWOQGNVFCVSMHEALHNHYTKLSLSPG 400
DB 628 RWOQGNVFCVSMHEALHNHYTKLSLSPG 658
RESULT 14
ADQ79910
ID ADQ79910 standard; protein; 659 AA.
XX
AC ADQ79910;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human tumour necrosis factor receptor 2, mgTNFR2-TNFR2/Ig construct.
XX
XX Human; tumour necrosis factor receptor; TNFR1; TNFR2; CTLA4; CD2; IgG;
KW immunoglobulin; concatameric fused dimer protein; immunoadhesin;
KW Fc fragment; hinge.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX KR2004009997-A.
PN
XX
PD 31-JAN-2004.
XX
XX
PF 26-JUL-2002; 2002KR-00045921.
XX
XX
PR 26-JUL-2002; 2002KR-00045921.
XX
XX (WEDE-) MEDEXGEN INC.
XX
XX Choi EY, Han JU, Jung YH, Kim JM, Lee HJ;
PI
XX WPI; 2004-458871/43.
DR N-PSDB; ADQ79909.
XX
XX Concatameric immunoadhesin.
PT
XX
PS Claim 27; SEQ ID NO 12; 129pp; Korean.
XX
XX The invention relates to a concatameric fused dimer protein and
CC glycosylation modification protein providing concatameric immunoadhesin
CC with improved efficacy and stability. The concatameric protein is
CC characteristically formed by binding C-terminal of one biologically
CC active protein with N-terminal of same or different biologically active
CC protein, e.g. tumour necrosis factor receptors (TNFR1 and TNFR2), CD2 and
CC CTLA4. Two monomer proteins which are formed by fusing the extracellular
CC region of a protein participating in the same immune reaction to an
CC immunoglobulin Fc fragment, bound together at a hinge region by
CC disulphide bond to give the concatameric fused dimer protein, wherein the
CC immunoglobulin is IgG. The present sequence represents a monomeric or


```
CC dimeric IgG fusion protein (or a dimeric fusion protein containing
XX engineered N-glycosylation sites, designated "mg").
SQ Sequence 659 AA;

Query Match      68.0%; Score 1522.5; DB 8; Length 659;
Best Local Similarity 65.4%; Pred. No. 1e-85;
Matches 295; Conservative 16; Mismatches 75; Indels 65; Gaps 5;

QY 9 HYDEETSHQLLCKPCPGTYLKQCHCTAKWKTVCAPCPDHYHYYTDSMHTSDCLYCSPVCKE 68
Db 214 YDQ--TAQWCCSKCSPGQHAQVFKTSDTVCDSCDSTYTQLMNNVPECLSGSRCS 271
QY 69 LQVVKQECNTHNRVCECKEGRYLEI-----BFLKHRSCPPGFGVVGAGTPERNTVCK 122
Db 272 DVETOACTREONRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARGTGTSDVVK 331
QY 123 RCPDGFESNETSKAPCRKHTNCSVFGLLLTQKGNATHDNIC----- 164
Db 332 PCAGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 387
QY 165 --SGNSESTQ-----KVDKTHTCPPCPAPELL 189
Db 388 PVSTRSQHTQTPSTAPSTFLLPMGPPPAEGSTGDAEPKSCDKTHTCPCPAPELL 447
QY 190 GPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQ 249
Db 448 GPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQ 507
QY 250 YNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 309
Db 508 YNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 567
QY 310 DELTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKS 369
Db 568 DELTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKS 627
QY 370 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPG 400
Db 628 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPG 658

RESULT 15
ADM32913
ID ADM32913 standard; protein; 489 AA.
XX
AC ADM32913;
XX
DT 17-JUN-2004 (first entry)
XX
DE Amino acid sequence of Enbrel (etanercept).
XX
KW synonymous codon; translation efficiency; Enbrel; etanercept.
XX
OS Synthetic.
XX
XX WO2004024915-A1.
XX
XX 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-AU001200.
XX
PR 13-SEP-2002; 2002US-0410410P.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Frazer IH;
XX
XX WPI; 2004-270043/25.
XX
DR N-PSDB; ADM32912, ADM32914.
XX
XX Constructing a synthetic polynucleotide, useful for producing a
PT polypeptide at a higher level in a Chinese Hamster Ovary cell, comprises
```

```
PT selecting a first codon of the parent polynucleotide for replacement with
PT a synonymous codon.
XX
XX Example 1; Fig 1; 82pp; English.
XX
CC The specification describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible at a different
CC level in a Chinese Hamster Ovary (CHO) cell compared to when using a
CC parent polynucleotide encoding the same polypeptide. The method comprises
CC selecting a first codon of the parent polynucleotide for replacement with
CC a synonymous codon, where the synonymous codon is selected on the basis
CC that it exhibits a different translational efficiency in the CHO cell
CC than the first codon in a comparison of translational efficiencies of
CC codons in test CHO cells. The method is useful for constructing synthetic
CC polynucleotides which are translated more efficiently, compared to the
CC parent polynucleotide. The present sequence represents Enbrel
CC (etanercept), a synthetic polynucleotide encoding a fusion protein
CC consisting of two soluble TNF receptors joined by the Fc fragment of a
CC human IgG1 molecule. The Enbrel polynucleotide was codon-modified, to
CC demonstrate the method of the invention.
XX
SQ Sequence 489 AA;
```

```
Query Match      67.7%; Score 1517; DB 8; Length 489;
Best Local Similarity 64.4%; Pred. No. 1.6e-85;
Matches 290; Conservative 20; Mismatches 76; Indels 64; Gaps 4;

QY 9 HYDEETSHQLLCKPCPGTYLKQCHCTAKWKTVCAPCPDHYHYYTDSMHTSDCLYCSPVCKE 68
Db 45 YDQ--TAQWCCSKCSPGQHAQVFKTSDTVCDSCDSTYTQLMNNVPECLSGSRCS 102
QY 69 LQVVKQECNTHNRVCECKEGRYLEI-----BFLKHRSCPPGFGVVGAGTPERNTVCK 122
Db 103 DVETOACTREONRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARGTGTSDVVK 162
QY 123 RCPDGFESNETSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS----- 168
Db 163 PCAGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 218
QY 169 -----ESTQKVDKTHTCPPCPAPELLG 278
Db 219 PVSTRSQHTQTPSTAPSTFLLPMGPPPAEGSTGDEPKSCDKTHTCPCPAPELLG 278
QY 191 GPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQ 250
Db 279 GPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQ 338
QY 251 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 310
Db 339 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 398
QY 311 ELTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 370
Db 399 EMTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 458
QY 371 WQOQGNVFCSCVMHEALHNHYTQKSLSLSPG 400
Db 459 WQOQGNVFCSCVMHEALHNHYTQKSLSLSPG 488
```

Search completed: March 8, 2005, 14:38:16
Job time : 85.8966 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:28:42 ; Search time 21.8688 Seconds
(without alignments)
1365.399 Million cell updates/sec

Title: US-09-389-782A-5
Perfect score: 2240
Sequence: 1 ETPPPKLYHDETSQLLC.....VMHEALHNHYTKSLSLSPG 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents RA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1510.5	67.4	486	US-08-243-010-1	Sequence 1, Appli
2	1502	67.1	518	US-08-385-229-4	Sequence 4, Appli
3	1502	67.1	518	US-09-579-845-1	Sequence 1, Appli
4	1502	67.1	518	US-09-579-845-3	Sequence 3, Appli
5	1352	60.4	360	US-09-180-100-11	Sequence 11, Appl
6	1352	60.4	376	US-09-180-100-22	Sequence 22, Appl
7	1345.5	60.1	398	US-09-612-033B-14	Sequence 14, Appl
8	1332	59.5	438	US-08-097-827-11	Sequence 11, Appl
9	1332	59.5	438	US-08-494-574-11	Sequence 11, Appl
10	1317.5	58.8	424	US-09-333-593A-8	Sequence 8, Appli
11	1266.5	56.5	911	US-08-484-438-10	Sequence 10, Appl
12	1252	55.9	704	US-09-590-656-2	Sequence 2, Appli
13	1252	55.9	704	US-09-733-764-2	Sequence 2, Appli
14	1249.5	55.8	664	US-08-957-063-16	Sequence 16, Appl
15	1249.5	55.8	664	US-09-487-685-16	Sequence 16, Appl
16	1249.5	55.8	664	US-08-802-805D-16	Sequence 16, Appl
17	1249.5	55.8	664	US-09-388-316C-16	Sequence 16, Appl
18	1248.5	55.7	664	US-08-957-063-18	Sequence 18, Appl
19	1248.5	55.7	664	US-09-487-685-18	Sequence 18, Appl
20	1248.5	55.7	664	US-08-802-805D-18	Sequence 18, Appl
21	1248.5	55.7	664	US-09-388-316C-18	Sequence 18, Appl
22	1247	55.7	397	US-09-854-864-18	Sequence 18, Appl
23	1245.5	55.6	283	US-09-854-864-9	Sequence 9, Appli
24	1245.5	55.6	482	US-09-189-129-2	Sequence 2, Appli
25	1245.5	55.6	482	US-09-824-286-2	Sequence 2, Appli
26	1245.5	55.6	680	US-08-227-496C-15	Sequence 15, Appl
27	1244.5	55.6	455	US-09-773-877B-24	Sequence 24, Appl

Sequence 23, Appli
Sequence 23, Appli
Sequence 8, Appli
Sequence 4, Appli
Sequence 54, Appli
Sequence 53, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 30, Appli
Sequence 43, Appli
Sequence 43, Appli

ALIGNMENTS

RESULT 1
US-08-243-010-1
; Sequence 1, Application US/08243010
; Patent No. 5639597
; GENERAL INFORMATION:
; APPLICANT: Lauffer, Leander
; APPLICANT: Zettlmeisel, Gerd
; APPLICANT: Oquendo, Patricia
; TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
; TITLE OF INVENTION: Production and Use Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,010
; FILING DATE: 13-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/798,564
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: DE P 40 37 837.3
; FILING DATE: 28-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 02481-1132-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 486 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-243-010-1

Query Match 67.4%; Score 1510.5; DB 1; Length 486;
Best Local Similarity 65.2%; Pred. No. 1.4e-118;

QY 69 LQYVQECNTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVGAGTPERNTVCK 122
DB 132 DQVETOACTREONRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARGTETSDVVC 191
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS----- 168
DB 192 PCAPGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTSTRMAPCAVHLPO 247
QY 169 -----ESTQKVDKTHTCPPCPAPPELLG 190
DB 248 PVSTRSQHTQTPPEPSTAPSTFLLPMGSPAPBAGSTGDEPKSCDKTHTCPPCPAPELLG 307
QY 191 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 250
DB 308 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 367
QY 251 NSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 310
DB 368 NSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 427
QY 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 370
DB 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487
QY 371 WQGNVFCSCVMHEALHNNHYTQKSLSPG 400
DB 488 WQGNVFCSCVMHEALHNNHYTQKSLSPG 517

RESULT 4

US-09-579-845-3

; Sequence 3, Application US/09579845

; Patent No. 6537540

; GENERAL INFORMATION:

; APPLICANT: Bursattein, Haim

; APPLICANT: Stepan, Anthony M.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING

; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED

; TITLE OF INVENTION: DISORDERS

; FILE REFERENCE: 226272004420

; CURRENT APPLICATION NUMBER: US/09/579,845

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 518

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-579-845-3

Query Match 67.18; Score 1502; DB 4; Length 518;
Best Local Similarity 63.84; Pred. No. 7.9e-118;
Matches 287; Conservative 21; Mismatches 78; Indels 64; Gaps 4;
QY 9 HYDEETSHQLLCKDCPPGTLYLKQHTAKWTVCAKPDHYVTSWHTSDECLYCSPVCKE 68
DB 74 YYDQ--TAQCCSKSCFGQHAQVFCTTSDTVCDSCDSTYTQLWNWVPECLSGSRCS 131
QY 69 LQYVQECNTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVGAGTPERNTVCK 122
DB 132 DQVETOACTREONRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARGTETSDVVC 191
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS----- 168
DB 192 PCAPGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTSTRMAPCAVHLPO 247
QY 169 -----ESTQKVDKTHTCPPCPAPPELLG 190
DB 248 PVSTRSQHTQTPPEPSTAPSTFLLPMGSPAPBAGSTGDEPKSCDKTHTCPPCPAPELLG 307

QY 191 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 250
DB 308 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 367
QY 251 NSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 310
DB 368 NSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 427
QY 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 370
DB 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487
QY 371 WQGNVFCSCVMHEALHNNHYTQKSLSPG 400
DB 488 WQGNVFCSCVMHEALHNNHYTQKSLSPG 517

RESULT 5

US-09-180-100-11

; Sequence 11, Application US/09180100

; Patent No. 6306395

; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, No. 63063951c

; APPLICANT: NAKAMURA, Shigekazu

; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE

; FILE REFERENCE: 1110-207P

; CURRENT APPLICATION NUMBER: US/09/180,100

; CURRENT FILING DATE: 1998-11-02

; EARLIER APPLICATION NUMBER: PCT/JP97/01502

; EARLIER FILING DATE: 1997-05-01

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-180-100-11

Query Match 60.44; Score 1352; DB 3; Length 360;
Best Local Similarity 67.3%; Pred. No. 1.9e-105;
Matches 270; Conservative 15; Mismatches 60; Indels 56; Gaps 9;
QY 8 LHYDEETSHQLLCKDCPPGTLYLKQHTAKW-KTVCAKCPD-HYVTSWHTSDECLYCSPV 65
DB 7 LHHDGQFCHK-PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFFSKRCR-L 61
QY 66 CKELQVVKOE--CNRTHNRVCECKEGRYLEIEFCLKHRSCPP---GFGVVGAGTPERNT 119
DB 62 CDEGHGLEVEINCTRTQNTKCRCKPNFFCNSTVC---EHCDCPTCKEHLIIECTLTSTNT 118
QY 120 VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKVDKHT 179
DB 119 KCKE--EGSRSNEPKS-----CDKTHT 138
QY 180 CPPCPAPPELLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 239
DB 139 CPPCPAPPELLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 198
QY 240 NAKTKPEREQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 299
DB 199 NAKTKPEREQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 258
QY 300 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 359
DB 259 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 318
QY 360 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSPG 400
DB 319 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSPG 359

RESULT 6

US-09-180-100-22

```
; Sequence 22, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAKAMURA, No. 630639510
; TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; EARLIER FILING DATE: 1998-11-02
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-22

Query Match      60.4%; Score 1352; DB 3; Length 376;
Best Local Similarity 67.3%; Pred. No. 2e-105;
Matches 270; Conservative 15; Mismatches 60; Indels 56; Gaps 9;

QY      8 LHYDETSHQLLDCRCPGTYLKHCHTAKW-KTVCACPD-HYTTDSWHTSDCLYCSVP 65
Db      23 LHHDCQFCHK-----PCPGERKARDCTVNGDEPCQCEGKEYTDKAFSSKRCR-L 77
QY      66 KLEQYVQOE--CNRTHNRVCECKEGRYLEIEFCLKHSRCP--EHCDPCTKCEHGIKCTLSNT 119
Db      78 CDEGHLEVEINCTRTQNTKCRCKPFCNSTVC---EHCDPCTKCEHGIKCTLSNT 134
QY      120 VKCRCPDGFENSTSSKAPCRKHTNCVFGLLLTQGNATHDNICSGNSESTOKVKTHT 179
Db      135 KCKE--EGSRNEPKS-----CDKTHT 154
QY      180 CPPCAPPELLGSPVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWVDGVVH 239
Db      155 CPPCAPPELLGSPVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWVDGVVH 214
QY      240 NAKTKPREOYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 299
Db      215 NAKTKPREOYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 274
QY      300 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 359
Db      275 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 334
QY      360 LYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSLSPG 400
Db      335 LYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSLSPG 375

RESULT 7
US-09-612-033B-14
; Sequence 14, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Sazis, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; FILE REFERENCE: of Genes
; CURRENT APPLICATION NUMBER: US/09/612,033B
; EARLIER FILING DATE: 2000-07-07
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: Immunoglobulin sequences
US-09-612-033B-14

Query Match      60.1%; Score 1345.5; DB 4; Length 398;
Best Local Similarity 67.7%; Pred. No. 7.6e-105;
Matches 264; Conservative 22; Mismatches 59; Indels 45; Gaps 7;

QY      12 EETSHQLLDCRCPGTYLKHCHTAKW-KTVCACPD-HYTTDSWHTSDCLYCSVPCKELQ 70
Db      52 EYWKDVCKNCAGTFVAPCEIPTHQCEKCHFGFTTEKNDYLDACILCS-TCDDKQ 110
QY      71 YVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPFGVQAGTPTERTVCKRCPDGPF 130
Db      111 EMVADCSATSDRKCQRTGLY-----YDKF-----PESCRPTCKCQ---- 149
QY      131 NETSSKAPCRKHTNCVFGLLLTQGNATHDNICSGNSESTOKVKTHTTCCPPAPPELLG 190
Db      150 -----GIPVLCNCSNTATVC---SSSVSNVD-THTCCPPAPPELLG 187
QY      191 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWVDGVVHNAKTTPREOY 250
Db      188 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWVDGVVHNAKTTPREOY 247
QY      251 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 310
Db      248 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 307
QY      311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYKSLTVDKSR 370
Db      308 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYKSLTVDKSR 367
QY      371 WQGNVFCSCVMHEALHNYTKQSLSLSPG 400
Db      368 WQGNVFCSCVMHEALHNYTKQSLSLSPG 397

RESULT 8
US-09-097-827-11
; Sequence 11, Application US/08097827
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
;               Goodwin, Ray
;               Fanslow, William
;               Gayle, Richard
; TITLE OF INVENTION: Novel Cytokine Which is a Ligand for
;               OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-Jul-1993
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
```

```
;
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-097-827-11

Query Match          59.5%; Score 1332; DB 1; Length 438;
Best Local Similarity 62.4%; Pred. No. 1.2e-103;
Matches 262; Conservative 23; Mismatches 75; Indels 60; Gaps 6;

QY 20 CDKCPGTYLKQCTAKWTKVACPCPDHYTD--SMHTSDECLYCSVCKELQYVQECN 77
DB 39 CRECPQGHGMVNRCDHTRDTLCHPCETGFYNEAVNYDTCKQCTQCNH--RSGSELKQNC 96
QY 78 RTHNRVCECKEGRYLEIEFLCKHRSCPPGFGVVQAGTPERTVCKRCPDGFFSNETSSKA 137
DB 97 PTQDTVCRCK-----PGTQPRQDSGYKLGVDVCPGPHFS--PCNNQ 137
QY 138 PCRKHNTCSVFGLLLTQKGNATHDNIICSGNS-----EST----- 171
DB 138 ACKPWNTCLSGKQTRHPASDSLDAVCEDRSLATLLWETQRTFRTPTTVQSTTVMPT 197
QY 172 -----QKVDKTHTCPPCPAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVVDV 220
DB 198 ELPSTPTLVPRSCDKTHTCPPCPAPPAEAGAPSVFLPPPKPDTLMISRTPEVTCVVVD 257
QY 221 SHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNK 280
DB 258 SHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNK 317
QY 281 ALPAPIEKTISKAKGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ 340
DB 318 ALPAPIEKTISKAKGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ 377
QY 341 PENNYKTTTPVLDSGDFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPG 400
DB 378 PENNYKTTTPVLDSGDFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPG 437

RESULT 9
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
```

```
;
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-494-574-11

Query Match          59.5%; Score 1332; DB 1; Length 438;
Best Local Similarity 62.4%; Pred. No. 1.2e-103;
Matches 262; Conservative 23; Mismatches 75; Indels 60; Gaps 6;

QY 20 CDKCPGTYLKQCTAKWTKVACPCPDHYTD--SMHTSDECLYCSVCKELQYVQECN 77
DB 39 CRECPQGHGMVNRCDHTRDTLCHPCETGFYNEAVNYDTCKQCTQCNH--RSGSELKQNC 96
QY 78 RTHNRVCECKEGRYLEIEFLCKHRSCPPGFGVVQAGTPERTVCKRCPDGFFSNETSSKA 137
DB 97 PTQDTVCRCK-----PGTQPRQDSGYKLGVDVCPGPHFS--PCNNQ 137
QY 138 PCRKHNTCSVFGLLLTQKGNATHDNIICSGNS-----EST----- 171
DB 138 ACKPWNTCLSGKQTRHPASDSLDAVCEDRSLATLLWETQRTFRTPTTVQSTTVMPT 197
QY 172 -----QKVDKTHTCPPCPAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVVDV 220
DB 198 ELPSTPTLVPRSCDKTHTCPPCPAPPAEAGAPSVFLPPPKPDTLMISRTPEVTCVVVD 257
QY 221 SHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNK 280
DB 258 SHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNK 317
QY 281 ALPAPIEKTISKAKGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ 340
DB 318 ALPAPIEKTISKAKGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ 377
QY 341 PENNYKTTTPVLDSGDFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPG 400
DB 378 PENNYKTTTPVLDSGDFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPG 437

RESULT 10
US-09-333-593A-8
; Sequence 8, Application US/09333593A
; Patent No. 6333269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 424
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
```

US-09-333-593A-8

Query Match 58.8%; Score 1317.5; DB 3; Length 424;
Best Local Similarity 68.1%; Pred. No. 1.9e-102;
Matches 261; Conservative 15; Mismatches 50; Indels 1

QY	23	CPPEYTLKHQCHTAKWKTVCAFCP-DHYITDSWHTSDDECLYCSPVCKELQVVKQBCNETHN	81
Db	81	CPPEGHHSIED-----GRDCISCKYGQDYSTQWMDLLFCLCRTR-CDSGEVELSPCTTTRN	134
QY	82	RVCECKEGRYLE---IFCCLKHRS-CPPGFGVQOAGTPERNVTCKRCPDGFFSNETSSKA	137
Db	135	TVQCEBGTFRBEDSPEMCRKCRGTCPRGMVKGVDCTPWSDIEC-----	178
QY	138	PCRKHTNCSYFGLLLTKQGNATHDNICSGNSESTQKVDKTHTCPCPCAPPELLCGSPSVFLP	197
Db	179	-VHKESGRSI-----EGRGTPKSAKTHTCPCPCAPPELLCGSPSVFLP	220
QY	198	PPPKOTLMTISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV	257
Db	221	PPPKOTLMTISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV	280
QY	258	SVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV	317
Db	281	SVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV	340
QY	318	SLTCLYKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNYP	377
Db	341	SLTCLYKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNYP	400
QY	378	SCSVMHEALHNHYTQKSLSLSPG	400
Db	401	SCSVMHEALHNHYTQKSLSLSPG	423

RESULT 11

US-08-484-438-10
 ; Sequence 10, Application US/08484438
 ; Patent No. 5811098
 ; Patent No. 5811098 5780031
 ; GENERAL INFORMATION:
 ; APPLICANT: PLOWMAN, Gregory D.
 ; APPLICANT: Culouscou, Jean-Michel
 ; APPLICANT: Shoyab, Mohammed
 ; APPLICANT: Siegall, Clay B.
 ; APPLICANT: Hellistr m, Ingegerd
 ; APPLICANT: Hellistr m, Karl E.
 ; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,438
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/323,442
 ; FILING DATE: 14-OCT-1994
 ; APPLICATION NUMBER: US 08/150,704
 ; FILING DATE: 10-NOV-1993
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/981,165

FILING DATE: 24-NOV-1992

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-438-10

Query Match 56.5%; Score 1266.5; DB 2; Length 911;
Best Local Similarity 59.6%; Pred. No. 9.9e-98;
Matches 267; Conservative 23; Mismatches 49; Indels 109; Gaps 16;

QY	31	QHCTAKWKTVCAPCDHYYTDS---WHTS--DECLYC-----SPVCKELQYVQKQECNRTHNR	82
Db	494	ENCTAE-GWVC-----NHLCSSDGCWGPGPQOCLSCRRFSRGRIC-----	534
QY	83	VECEKEGRYLIE---FCLKHSRCPFGVQVQAGT-----PERTVC-----	K 122
Db	535	SNLYDGEFRFENGSLCIVE---CDPOCEKMEGLLTCHGPGDNCCKSHFKDGNPCVFE	591
QY	123	RCPDGF-----FSNETSKAPCRKHTKNCVFGLLLTQ---KGNATHDNI---CSGNS	168
Db	592	KCPDGLQAGANSFIKYADPDRECHPC--HFNC-----TQCGNGPSTSHDCIYYPWTGHS	642
QY	169	-----ESTQKVDKTHCTPPCPAPPELLGCP	192
Db	643	TLPODPVKVKALEGFPRLVGDPFFGCAEPANTFLDPEPRKCDKTHCTPPCPAPPELLGCP	702
QY	193	SVFLFPKPKDTLMSIRTPVTCVVDVSHEDDEVKFNWVDGVEVHNAKTKPREEOYNS	252
Db	703	SVFLFPKPKDTLMSIRTPVTCVVDVSHEDDEVKFNWVDGVEVHNAKTKPREEOYNS	762
QY	253	TYRVVSVLTVLHDWLNKGEYKCKVNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL	312
Db	763	TYRVVSVLTVLHDWLNKGEYKCKVNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL	822
QY	313	TKNQVSLTCLVKGFYPSDIAVESHESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRM	372
Db	823	TKNQVSLTCLVKGFYPSDIAVESHESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRM	882
QY	373	QGNVFCSVNHAEALHNHYTQKSLSLSPG	400
Db	883	QGNVFCSVNHAEALHNHYTQKSLSLSPG	910

RESULT 12

```

US-09-590-656-2
; Sequence 2, Application US/09590656
; Patent No. 6413932
; GENERAL INFORMATION:
; APPLICANT: Carretti, Douglas P.
; APPLICANT: Borges, Luis G.
; APPLICANT: Fanslow, III, William C.
; TITLE OF INVENTION: TEK ANTAGONISTS
; FILE REFERENCE: 2900-A
; CURRENT APPLICATION NUMBER: US/09/590,656
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/137,889
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

```


Best Local Similarity 63.6%; Pred. No. 1.7e-96;
Matches 264; Conservative 23; Mismatches 57; Indels 71; Gaps 14;

QY	32	HCTAKWKTVCACP--DHY-----	YTDWHTSDCLYCSVPCKELQV 72
Db	274	NCRASYQIVTS--CPADNYOACLGSVAGMIGFDMTPNYVDSPTG--IVVSPWC-----	323
QY	73	KQECNRTHNRVCECKEGRYLEIEF-----CLKH-----	RSCP--PGFVVQAGTP 115
Db	324	--SCRGSGNMBEECE--KFLR--DFTENPCLRNAIQAFNGTDMVNSPKGFSQATQAPRV 378	
QY	116	ERNVCKRCPDGFFSNETSCKAPCKHTNCSVFGLLLTQKNATHD-----NICS 165	
Db	379	EKT---PSLPDDLSDSTSLGTSVITCTSVQEOGL-----KANNSKELSMCFTELTNTIIP 431	
QY	166	GNSESTQKVDKTHTCPPCPAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDP 225	
Db	432	GPDR---PVDKTHTCPPCPAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDP 488	
QY	226	EVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNMGKEYCKVSNKALPAP 285	
Db	489	EVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNMGKEYCKVSNKALPAP 548	
QY	286	IEKTIISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 345	
Db	549	IEKTIISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 608	
QY	346	KTTTPVLDSGSPFLYSLKLTVDKSRWQGNVFCVSMHEALHNYHTQKSLSPG 400	
Db	609	KTTTPVLDSGSPFLYSLKLTVDKSRWQGNVFCVSMHEALHNYHTQKSLSPG 663	

RESULT 15

US-09-487-685-16

; Sequence 16, Application US/09487685

; Patent No. 6342348

; GENERAL INFORMATION:

; APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes

; TITLE OF INVENTION: Neurturin Receptor

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/487,685

; FILING DATE: 19-Jan-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/957,063

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 913

; FILING DATE: 18-Feb-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, Ph.D., Timothy E.

; REGISTRATION NUMBER: 36,700

; REFERENCE/DOCKET NUMBER: P1086P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 664 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-487-685-16

Query Match 55.8%; Score 1249.5; DB 3; Length 664;

Best Local Similarity 63.6%; Pred. No. 1.7e-96;

Matches 264; Conservative 23; Mismatches 57; Indels 71; Gaps 14;

QY	32	HCTAKWKTVCACP--DHY-----	YTDWHTSDCLYCSVPCKELQV 72
----	----	-------------------------	--------------------------

Db	274	NCRASYQIVTS--CPADNYOACLGSVAGMIGFDMTPNYVDSPTG--IVVSPWC-----	323
----	-----	--	-----

QY	73	KQECNRTHNRVCECKEGRYLEIEF-----CLKH-----	RSCP--PGFVVQAGTP 115
----	----	--	----------------------

Db	324	--SCRGSGNMBEECE--KFLR--DFTENPCLRNAIQAFNGTDMVNSPKGFSQATQAPRV 378	
----	-----	---	--

QY	116	ERNVCKRCPDGFFSNETSCKAPCKHTNCSVFGLLLTQKNATHD-----NICS 165	
----	-----	--	--

Db	379	EKT---PSLPDDLSDSTSLGTSVITCTSVQEOGL-----KANNSKELSMCFTELTNTIIP 431	
----	-----	--	--

QY	166	GNSESTQKVDKTHTCPPCPAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDP 225	
----	-----	--	--

Db	432	GPDR---PVDKTHTCPPCPAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDP 488	
----	-----	--	--

QY	226	EVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNMGKEYCKVSNKALPAP 285	
----	-----	--	--

Db	489	EVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNMGKEYCKVSNKALPAP 548	
----	-----	--	--

QY	286	IEKTIISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 345	
----	-----	---	--

Db	549	IEKTIISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 608	
----	-----	---	--

QY	346	KTTTPVLDSGSPFLYSLKLTVDKSRWQGNVFCVSMHEALHNYHTQKSLSPG 400	
----	-----	---	--

Db	609	KTTTPVLDSGSPFLYSLKLTVDKSRWQGNVFCVSMHEALHNYHTQKSLSPG 663	
----	-----	---	--

Search completed: March 8, 2005, 14:48:11

Job time : 23.8688 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:44:50 ; Search time 60.4374 Seconds
(without alignments)
2177.757 Million cell updates/sec

Title: US-09-389-782a-5

Perfect score: 2240

Sequence: 1 ETFFPKYLYHDETSQQLLC.....VMHEALHNYTQKLSLSLSPG 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTU5_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2240	100.0	400	10	US-09-389-782-5
2	2227	99.4	406	10	US-09-389-782-6
3	2225	99.3	425	16	US-10-467-243-20
4	2222.5	99.2	407	10	US-09-389-782-3
5	2218.5	99.0	413	10	US-09-389-782-4
6	2191	97.8	404	10	US-09-389-782-7
7	1522.5	68.0	659	14	US-10-363-427-12
8	1517	67.7	467	17	US-10-901-735-4
9	1514.5	67.6	490	14	US-10-363-427-4
10	1514.5	67.6	720	14	US-10-363-427-8
11	1502	67.1	518	14	US-10-313-852-1
12	1502	67.1	518	14	US-10-313-852-3
13	1502	67.1	518	14	US-10-314-033-1
					Sequence 5, Appli
					Sequence 6, Appli
					Sequence 20, Appli
					Sequence 3, Appli
					Sequence 4, Appli
					Sequence 7, Appli
					Sequence 12, Appli
					Sequence 4, Appli
					Sequence 8, Appli
					Sequence 1, Appli
					Sequence 3, Appli

14	1502	67.1	518	14	US-10-314-033-3	Sequence 3, Appli
15	1502	67.1	518	15	US-10-423-507-1	Sequence 1, Appli
16	1461.5	65.2	443	14	US-10-151-071-5	Sequence 5, Appli
17	1461.5	65.2	443	14	US-10-166-232A-5	Sequence 5, Appli
18	1459.5	65.2	444	16	US-10-467-243-24	Sequence 24, Appli
19	1392.5	62.2	608	14	US-10-363-427-10	Sequence 10, Appli
20	1384.5	61.8	444	14	US-10-363-427-2	Sequence 2, Appli
21	1384.5	61.8	628	14	US-10-363-427-6	Sequence 6, Appli
22	1352	60.4	360	9	US-09-949-713-11	Sequence 11, Appli
23	1352	60.4	376	9	US-09-949-713-22	Sequence 22, Appli
24	1352	60.4	376	14	US-10-084-139-10	Sequence 10, Appli
25	1350.5	60.3	396	14	US-10-193-616-14	Sequence 14, Appli
26	1345.5	60.1	398	15	US-10-622-407-14	Sequence 14, Appli
27	1283.5	57.3	380	9	US-09-948-018-39	Sequence 39, Appli
28	1280	57.1	446	9	US-09-792-2008-10	Sequence 10, Appli
29	1273	56.8	404	9	US-09-948-018-16	Sequence 16, Appli
30	1267	56.6	360	15	US-10-390-566-20	Sequence 20, Appli
31	1267	56.6	360	15	US-10-390-566-27	Sequence 27, Appli
32	1267	56.6	367	15	US-10-390-566-19	Sequence 19, Appli
33	1267	56.6	367	15	US-10-390-566-26	Sequence 26, Appli
34	1266	56.5	360	15	US-10-390-566-7	Sequence 7, Appli
35	1266	56.5	360	15	US-10-390-566-6	Sequence 6, Appli
36	1266	56.5	367	15	US-10-390-566-13	Sequence 13, Appli
37	1266	56.5	367	15	US-10-390-566-16	Sequence 16, Appli
38	1264	56.4	542	9	US-09-792-2008-16	Sequence 36, Appli
39	1257	56.1	380	9	US-09-948-018-36	Sequence 15, Appli
40	1257	56.1	404	15	US-10-258-368-15	Sequence 8, Appli
41	1256	56.1	334	15	US-10-258-368-8	Sequence 6, Appli
42	1256	56.1	366	15	US-10-258-368-6	Sequence 15, Appli
43	1254.5	56.0	810	14	US-10-232-838-15	Sequence 17, Appli
44	1254.5	56.0	934	14	US-10-232-838-17	Sequence 18, Appli
45	1254.5	56.0	949	14	US-10-232-838-18	

ALIGNMENTS

RESULT 1
US-09-389-782-5
; Sequence 5, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-5

Query Match 100.0%; Score 2240; DB 10; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.2e-141;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ETFFPKYLYHDETSQQLLCDCPCPGTYLKQHTAKWTVCAPCPDHYTDSNHTSDECL	60
DB	1	ETFFPKYLYHDETSQQLLCDCPCPGTYLKQHTAKWTVCAPCPDHYTDSNHTSDECL	60
QY	61	YCSVPCKELOYKQSCNRTHNRVCSCKEGRYLEIFECLEKHSRCPGFGVVGAGTPTERTV	120
DB	61	YCSVPCKELOYKQSCNRTHNRVCSCKEGRYLEIFECLEKHSRCPGFGVVGAGTPTERTV	120
QY	121	CKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSTQKVDKHTC	180
DB	121	CKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSTQKVDKHTC	180

QY 181 PPCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHN 240
Db 181 PPCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHN 240
QY 241 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 300
Db 241 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 300
QY 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLL 360
Db 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLL 360
QY 361 YSKLTVDKSRWQOGNVPFSCVMHRLAHNYTKQSLSPG 400
Db 361 YSKLTVDKSRWQOGNVPFSCVMHRLAHNYTKQSLSPG 400

RESULT 2
US-09-389-782-6
; Sequence 6, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Holdings Ltd.
; APPLICANT: Haaning, Jesper Mortensen
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES
; FILE REFERENCE: 0226w0310
; CURRENT APPLICATION NUMBER: US/10/467,243
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: DK PA 2001 00214
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/267,843
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00498
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/278,320
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPG-Fc polypeptide encoded by SEQ ID NO:19
US-10-467-243-20

Query Match 99.4%; Score 2227; DB 10; Length 406;
Best Local Similarity 98.5%; Pred. No. 3.1e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
QY 1 ETPPKYLHYDEETSHQLLCKDCKPPGTYLKQCTAKWTVCAPCPDHYTDSWHTSDECL 60
Db 1 ETPPKYLHYDEETSHQLLCKDCKPPGTYLKQCTAKWTVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPERNTV 120
Db 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPERNTV 120
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQK-----V 174
Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQK-----V 174
QY 175 DKHTTCCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 234
Db 181 DKHTTCCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
QY 235 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 294
Db 241 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
QY 295 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD 354
Db 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD 360
QY 355 DGSFELYSKLTVDKSRWQOGNVPFSCVMHRLAHNYTKQSLSPG 400
Db 361 DGSFELYSKLTVDKSRWQOGNVPFSCVMHRLAHNYTKQSLSPG 406

RESULT 3
US-10-467-243-20
; Sequence 20, Application US/10467243

Publication No. US20040132971A1
GENERAL INFORMATION:
APPLICANT: Maxygen Holdings Ltd.
APPLICANT: Haaning, Jesper Mortensen
APPLICANT: Halkier, Torben
TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES
FILE REFERENCE: 0226w0310
CURRENT APPLICATION NUMBER: US/10/467,243
CURRENT FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: DK PA 2001 00214
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/267,843
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: DK PA 2001 00498
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/278,320
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 425
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: OPG-Fc polypeptide encoded by SEQ ID NO:19
US-10-467-243-20

Query Match 99.3%; Score 2225; DB 16; Length 425;
Best Local Similarity 98.8%; Pred. No. 4.5e-140;
Matches 399; Conservative 1; Mismatches 0; Indels 4; Gaps 1;
QY 1 ETPPKYLHYDEETSHQLLCKDCKPPGTYLKQCTAKWTVCAPCPDHYTDSWHTSDECL 60
Db 22 ETPPKYLHYDEETSHQLLCKDCKPPGTYLKQCTAKWTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPERNTV 120
Db 82 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPERNTV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQK-----DK 176
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQKLEKSSDK 201
QY 177 THTCPPCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 236
Db 202 THTCPPCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 261
QY 237 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 296
Db 262 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 321
QY 297 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 356
Db 322 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 381
QY 357 SFFLYSLKLTVDKSRWQOGNVPFSCVMHRLAHNYTKQSLSPG 400
Db 382 SFFLYSLKLTVDKSRWQOGNVPFSCVMHRLAHNYTKQSLSPG 425

RESULT 4
US-09-389-782-3
; Sequence 3, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-3

Query Match      99.2%; Score 2222.5; DB 10; Length 407;
Best Local Similarity 98.0%; Pred. No. 6.3e-140;
Matches 399; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

Qy 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Qy 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVWQAGTPERTNV 120
Db 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVWQAGTPERTNV 120
Qy 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKV----- 174
Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKAAABPKS 180
Qy 175 -DKTHTCCPCPAPELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 233
Db 181 CDKTHTCPCPAPELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 240
Qy 234 DGVEVHNKTKPREEQNSTYRVVSVLTJLHODWLNKGYCKVSNKALPAPIEKTISKA 293
Db 241 DGVEVHNKTKPREEQNSTYRVVSVLTJLHODWLNKGYCKVSNKALPAPIEKTISKA 300
Qy 294 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 353
Db 301 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
Qy 354 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 400
Db 361 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 407

RESULT 5
US-09-389-782-4
; Sequence 4, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-4

Query Match      99.0%; Score 2218.5; DB 10; Length 413;
Best Local Similarity 96.6%; Pred. No. 1.2e-139;
Matches 399; Conservative 0; Mismatches 1; Indels 13; Gaps 1;

Qy 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Qy 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVWQAGTPERTNV 120
Db 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVWQAGTPERTNV 120
Qy 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQK----- 173
Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQK----- 173

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-3

Query Match      99.2%; Score 2222.5; DB 10; Length 407;
Best Local Similarity 98.0%; Pred. No. 6.3e-140;
Matches 399; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

Qy 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Qy 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVWQAGTPERTNV 120
Db 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVWQAGTPERTNV 120
Qy 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKV----- 174
Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKAAABPKS 180
Qy 175 -DKTHTCCPCPAPELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 233
Db 181 CDKTHTCPCPAPELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 240
Qy 234 DGVEVHNKTKPREEQNSTYRVVSVLTJLHODWLNKGYCKVSNKALPAPIEKTISKA 293
Db 241 DGVEVHNKTKPREEQNSTYRVVSVLTJLHODWLNKGYCKVSNKALPAPIEKTISKA 300
Qy 294 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 353
Db 301 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
Qy 354 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 400
Db 361 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 407

RESULT 6
US-09-389-782-7
; Sequence 7, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-7

Query Match      97.8%; Score 2191; DB 10; Length 404;
Best Local Similarity 97.8%; Pred. No. 7.7e-138;
Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

Qy 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Qy 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVWQAGTPERTNV 120
Db 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVWQAGTPERTNV 120
Qy 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKV---DK 176
Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGG 180
Qy 177 THTCPCPAPELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 236
Db 181 GGTCCPCPAPELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 240
Qy 237 EVHNKTKPREEQNSTYRVVSVLTJLHODWLNKGYCKVSNKALPAPIEKTISKAQ 296
Db 241 EVHNKTKPREEQNSTYRVVSVLTJLHODWLNKGYCKVSNKALPAPIEKTISKAQ 300
Qy 297 PREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 356
Db 301 PREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 360
Qy 357 SFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 400
Db 361 SFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 404
```

RESULT 7

US-10-363-427-12
; Sequence 12, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: MedExGen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatametric Immunoadhesion
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 12
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-427-12

Query Match 68.0%; Score 1522.5; DB 14; Length 659;
Best Local Similarity 65.4%; Pred. No. 4e-93;
Matches 295; Conservative 16; Mismatches 75; Indels 65; Gaps 5;

QY 9 HYDEETSHQLCDKCPPTGTYLKQHTAKWKTVCAPCPDHYHYTDSWHTSDCLCYCSPVCKE 68
Db 214 YYDQ--TAQMCCKSCSPGQAHKVFCTKTSITVDCSCDSTYTQLNNWVPECLSGRCSS 271
QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFCLKHSRCPGPGVVGAGTPERNTVCK 122
Db 272 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVCK 331
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC-----164
Db 332 PCAPGTFTNTSSDTCRPHQICNVVAI-----PQNASMDAVCTSTPTSRMAPGAVHLPQ 387
QY 165 --SGNSSTQ-----KVDKTHTCPPCPAPPELL 189
Db 388 PVSTRSQHTQTPPEPSTAPSTSFLLPMGSPPAEGSTGDAEPKSCDKTHTCCPAPPELL 447
QY 190 GGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQ 249
Db 448 GGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQ 507
QY 250 YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 309
Db 508 YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 567
QY 310 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 369
Db 568 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 627
QY 370 RWOQGNVFCVSNMHEALHNHYTQKSLSLSPG 400
Db 628 RWOQGNVFCVSNMHEALHNHYTQKSLSLSPG 658

RESULT 8

US-10-901-735-4
; Sequence 4, Application US/10901735
; Publication No. US20050032183A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN, Inc.
; APPLICANT: OSSUND, Timothy D.
; APPLICANT: CLOSTON, Christi
; APPLICANT: CRAMPTON, Shon
; APPLICANT: BASS, Randal
; TITLE OF INVENTION: CRYSTALLINE POLYPEPTIDES
; FILE REFERENCE: A-859

; CURRENT APPLICATION NUMBER: US/10/901,735
; CURRENT FILING DATE: 2004-07-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide
US-10-901-735-4

Query Match 67.7%; Score 1517; DB 17; Length 467;
Best Local Similarity 64.4%; Pred. No. 6.3e-93;
Matches 290; Conservative 20; Mismatches 76; Indels 64; Gaps 4;

QY 9 HYDEETSHQLCDKCPPTGTYLKQHTAKWKTVCAPCPDHYHYTDSWHTSDCLCYCSPVCKE 68
Db 23 YYDQ--TAQMCCKSCSPGQAHKVFCTKTSITVDCSCDSTYTQLNNWVPECLSGRCSS 80
QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFCLKHSRCPGPGVVGAGTPERNTVCK 122
Db 81 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVCK 140
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS-----168
Db 141 PCAPGTFTNTSSDTCRPHQICNVVAI-----PQNASMDAVCTSTPTSRMAPGAVHLPQ 196
QY 169 -----ESTQKVDKTHTCPPCPAPPELLG 190
Db 197 PVSTRSQHTQTPPEPSTAPSTSFLLPMGSPPAEGSTGDEPKSCDKTHTCCPAPPELLG 256
QY 191 GGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQ 250
Db 257 GGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQ 316
QY 251 NSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 310
Db 317 NSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 376
QY 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 370
Db 377 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 436
QY 371 WQOQGNVFCVSNMHEALHNHYTQKSLSLSPG 400
Db 437 WQOQGNVFCVSNMHEALHNHYTQKSLSLSPG 466

RESULT 9

US-10-363-427-4
; Sequence 4, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: MedExGen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatametric Immunoadhesion
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 4
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-427-4

```
Query Match      67.6%; Score 1514.5; DB 14; Length 490;
Best Local Similarity 65.2%; Pred. No. 9.8e-93;
Matches 294; Conservative 16; Mismatches 76; Indels 65; Gaps 5;

QY 9 HYDETSQHLCDKCPGTYLKHQCTAKWKTVCAPCPDHYHVTDSWHTSDECLYCSPVCKE 68
DB 45 YYDQ--TAQMCCKSCSGQAHKVFCTKTSVTDCSDSTYTQLMNVPECLSCGSRCS 102

QY 69 LOYVQECNTHNRVCECKEGRYLEI-----EFLKHSRCPGFGVVOAGTPERNTVCK 122
DB 103 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARPGTETSDVCK 162

QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC----- 164
DB 163 PCAPGTFSNTSSTDCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 218

QY 165 --SGNSESTQ-----KVDKTHTCPPCPAPELL 189
DB 219 PVSTRSQHTQTPPEPSTAPSTSFLLPMGPPPAEGSTGDAEPKSCDKTHTCCPPAPELL 278

QY 190 GSPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 249
DB 279 GSPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 338

QY 250 YNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 309
DB 339 YNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 398

QY 310 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 369
DB 399 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 458

QY 370 RWQGNVFCSCVMHEALHNHYTQKSLSLSPG 400
DB 459 RWQGNVFCSCVMHEALHNHYTQKSLSLSPG 489

RESULT 10
US-10-363-427-8
; Sequence 8, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: MedGen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatametric Immunoadhesion
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 8
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-427-8

Query Match      67.6%; Score 1514.5; DB 14; Length 720;
Best Local Similarity 65.2%; Pred. No. 1.5e-92;
Matches 294; Conservative 16; Mismatches 76; Indels 65; Gaps 5;

QY 9 HYDETSQHLCDKCPGTYLKHQCTAKWKTVCAPCPDHYHVTDSWHTSDECLYCSPVCKE 68
DB 275 YYDQ--TAQMCCKSCSGQAHKVFCTKTSVTDCSDSTYTQLMNVPECLSCGSRCS 332

QY 69 LOYVQECNTHNRVCECKEGRYLEI-----EFLKHSRCPGFGVVOAGTPERNTVCK 122
DB 333 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARPGTETSDVCK 392
```

```
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC----- 164
DB 393 PCAPGTFSNTSSTDCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 448

QY 165 --SGNSESTQ-----KVDKTHTCPPCPAPELL 189
DB 449 PVSTRSQHTQTPPEPSTAPSTSFLLPMGPPPAEGSTGDAEPKSCDKTHTCCPPAPELL 508

QY 190 GSPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 249
DB 509 GSPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 568

QY 250 YNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 309
DB 569 YNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 628

QY 310 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 369
DB 629 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 688

QY 370 RWQGNVFCSCVMHEALHNHYTQKSLSLSPG 400
DB 689 RWQGNVFCSCVMHEALHNHYTQKSLSLSPG 719

RESULT 11
US-10-313-852-1
; Sequence 1, Application US/10313852
; Publication No. US20030103942A1
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 22627200420
; CURRENT APPLICATION NUMBER: US/10/313,852
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-313-852-1

Query Match      67.1%; Score 1502; DB 14; Length 518;
Best Local Similarity 63.8%; Pred. No. 7.1e-92;
Matches 287; Conservative 21; Mismatches 78; Indels 64; Gaps 4;

QY 9 HYDETSQHLCDKCPGTYLKHQCTAKWKTVCAPCPDHYHVTDSWHTSDECLYCSPVCKE 68
DB 74 YYDQ--TAQMCCKSCSGQAHKVFCTKTSVTDCSDSTYTQLMNVPECLSCGSRCS 131

QY 69 LOYVQECNTHNRVCECKEGRYLEI-----EFLKHSRCPGFGVVOAGTPERNTVCK 122
DB 132 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARPGTETSDVCK 191

QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS----- 168
DB 192 PCAPGTFSNTSSTDCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247

QY 169 -----ESTQKDKTHTCPPCPAPELL 190
DB 248 PVSTRSQHTQTPPEPSTAPSTSFLLPMGPPPAEGSTGDEPKSCDKTHTCCPPAPELL 307

QY 191 GSPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 250
DB 308 GSPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 367
```



```
QY 251 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 310
Db 368 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPMQKTIISKAKGQPREPOVYTLPPSRD 427
QY 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 370
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 487
QY 371 WQGNVFSCSVMEALHNHYTQKSLSLSPG 400
Db 488 WQGNVFSCSVMEALHNHYTQKSLSLSPG 517

RESULT 12
US-10-313-852-3
; Sequence 3, Application US/10313852
; Publication No. US20030103942A1
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/313,852
; CURRENT FILING DATE: 2002-12-06
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-313-852-3

Query Match 67.1%; Score 1502; DB 14; Length 518;
Best Local Similarity 63.8%; Pred. No. 7,1e-92;
Matches 287; Conservative 21; Mismatches 78; Indels 64; Gaps 4;

QY 9 HYDEETSHQLLCKCPGGTYLKQCTAKWKVCAPCPDHYHDTSDWHTSDRCLYCSPVCKE 68
Db 74 YDQ--TAQCCSKCSPGQAKVFCSTSDTCDSCEDSTYTQLMNNWPECLSCGSRCS 131
QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFLCKHRSCPPGFGVVOAGTPERNVTCK 122
Db 132 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARGTETSDVCK 191
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHNICSGNS-----168
Db 192 PCAPGTFTNTSTDCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247
QY 169 -----ESTQKVDKTHTCPCPAPELLG 190
Db 248 PVSTRSQHTQTPPEPSTAPSTFLLPMGPPSPABSGTGDEPKSCDKTHTCPCPAPELLG 307
QY 191 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 250
Db 308 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 367
QY 251 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 310
Db 368 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPMQKTIISKAKGQPREPOVYTLPPSRD 427
QY 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 370
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 487
QY 371 WQGNVFSCSVMEALHNHYTQKSLSLSPG 400
Db 488 WQGNVFSCSVMEALHNHYTQKSLSLSPG 517

RESULT 14
US-10-314-033-3
; Sequence 3, Application US/10314033
; Publication No. US20030113295A1
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
```

```
Db 488 WQGNVFSCSVMEALHNHYTQKSLSLSPG 517

RESULT 13
US-10-314-033-1
; Sequence 1, Application US/10314033
; Publication No. US20030113295A1
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/314,033
; CURRENT FILING DATE: 2002-12-06
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-033-1

Query Match 67.1%; Score 1502; DB 14; Length 518;
Best Local Similarity 63.8%; Pred. No. 7,1e-92;
Matches 287; Conservative 21; Mismatches 78; Indels 64; Gaps 4;

QY 9 HYDEETSHQLLCKCPGGTYLKQCTAKWKVCAPCPDHYHDTSDWHTSDRCLYCSPVCKE 68
Db 74 YDQ--TAQCCSKCSPGQAKVFCSTSDTCDSCEDSTYTQLMNNWPECLSCGSRCS 131
QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFLCKHRSCPPGFGVVOAGTPERNVTCK 122
Db 132 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARGTETSDVCK 191
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHNICSGNS-----168
Db 192 PCAPGTFTNTSTDCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247
QY 169 -----ESTQKVDKTHTCPCPAPELLG 190
Db 248 PVSTRSQHTQTPPEPSTAPSTFLLPMGPPSPABSGTGDEPKSCDKTHTCPCPAPELLG 307
QY 191 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 250
Db 308 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 367
QY 251 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 310
Db 368 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPMQKTIISKAKGQPREPOVYTLPPSRD 427
QY 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 370
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 487
QY 371 WQGNVFSCSVMEALHNHYTQKSLSLSPG 400
Db 488 WQGNVFSCSVMEALHNHYTQKSLSLSPG 517

RESULT 14
US-10-314-033-3
; Sequence 3, Application US/10314033
; Publication No. US20030113295A1
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:20:42 ; Search time 16.3022 Seconds
(without alignments)
2360.831 Million cell updates/sec

Title: US-09-389-782a-5
Perfect score: 2240
Sequence: 1 ETFPKYLHYDETSQLLC.....VMHEALNHVYTKLSLSLSPG 400
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	55.1	330	1 GHU	Ig gamma-1 chain C
2	1229	54.9	255	4 S31866	Ig gamma-1 chain C
3	1225	54.7	374	2 S69339	Ig heavy chain V x
4	1183.5	52.8	234	2 PT0207	Ig gamma chain C x
5	1154.5	51.5	377	2 A23511	Ig gamma-3 chain C
6	1152.5	51.5	377	2 A60764	Ig gamma-3 chain C
7	1148.5	51.3	326	1 G2HU	Ig gamma-2 chain C
8	1136	50.7	327	1 G4HU	Ig gamma-4 chain C
9	1133.5	50.6	289	1 G3HUI	Ig gamma-3 heavy C
10	923	41.2	323	1 GHRB	Ig gamma chain C x
11	917.5	41.0	348	2 I47160	Ig gamma 2b chain
12	917.5	41.0	328	2 I47159	Ig gamma 2a chain
13	915.5	40.9	277	2 I47162	Ig gamma 4 chain C
14	904.5	40.4	329	1 G2GP	Ig gamma-2 chain C
15	895.5	40.0	328	2 I47158	Ig gamma-1 chain c
16	889.5	39.7	328	2 I47161	Ig gamma 3 chain c
17	861.5	38.5	470	2 S22080	Ig heavy chain pre
18	851.5	38.0	308	2 C30554	Ig heavy chain C x
19	851.5	38.0	472	2 S31459	Ig gamma-1 chain -
20	847.5	37.8	329	1 G3MSC	Ig gamma-3 chain C
21	843	37.6	333	2 PS0018	Ig gamma-2b chain
22	841.5	37.6	338	1 G3MSM	Ig gamma-3 chain C
23	830	37.1	444	2 FC436	monoclonal antibody
24	820	36.6	324	1 G1MS	Ig gamma-1 chain C
25	820	36.6	326	2 PS0017	Ig gamma-1 chain C
26	820	36.6	393	1 G1MSM	Ig gamma-1 chain C
27	812.5	36.3	330	1 G2MSA	Ig gamma-2a chain
28	812.5	36.3	339	1 G2MSAM	Ig gamma-2a chain
29	812.5	36.3	469	2 S37483	Ig gamma-2a chain

RESULT 1

GHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; S33861; S33887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: UNIPROT:P01857; EMBL:Z17370

A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers,

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:Z17370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A;Reference number: S33887; MUID:83001943; PMID:6811139

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutschauer, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C.

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A;Reference number: A90563; MUID:71064024; PMID:5489771

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96, 'R', 98-135 <CUN>

A;Note: this sequence has the Glm(3) marker, 97-Arg

R;Rutschauer, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A;Reference number: A90564; MUID:71064025; PMID:5530842

A;Contents: Eu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,

A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met

R;Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primaerstruktur.

A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:93289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMI>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 55.1%; Score 1234; DB 1; Length 330;

Best Local Similarity 92.1%; Pred. No. 7.1e-68;

Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;

QY 159 THDNICS-----GNSESTOKV-----DKTHTCPCPAPPELLGGPSVFLFPPPKDTLMIS 208

DB 78 TQYICNNVHKPSNTKVDKKVFKPSCKDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMIS 137

QY 209 RTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 268

DB 138 RTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 197

QY 269 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYF 328

DB 198 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYF 257

QY 329 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN 388

DB 258 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN 317

QY 389 HYTKSLSLSPG 400

DB 318 HYTKSLSLSPG 329

RESULT 2

Ig gamma-1 chain C region - synthetic

C;Species: synthetic

A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
R;Accession: S31866
R;Filpula, D.

submitted to the EMBL Data Library, February 1993

A;Description: Screening method for protein-protein interactions of cloned gene products.

A;Reference number: S31866

A;Accession: S31866

A;Molecule type: mRNA

A;Residues: 1-255 <FIL>

A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069

C;Keywords: immunoglobulin

F;1-22/Region: Escherichia coli outer membrane protein A precursor

F;23-255/Region: human Ig gamma-1 chain C region

Query Match 54.9%; Score 1229; DB 4; Length 255;

Best Local Similarity 98.3%; Pred. No. 1.1e-67;

Matches 226; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 171 TQVVDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 230

DB 25 SKSCDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 84

QY 231 WYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 290

DB 85 WYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 144

QY 291 SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTTP 350

DB 145 SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTTP 204

QY 351 VLDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKSLSLSPG 400

DB 205 VLDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKSLSLSPG 254

RESULT 3

Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C;Accession: S69339; S72664

R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A;Reference number: S69339; MUID:95262687; PMID:7744049

A;Accession: S69339

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-374 <KHA>

A;Cross-references: EMBL:X81695

R;Khamlichi, A.A.

submitted to the EMBL Data Library, September 1994

A;Reference number: S72664

A;Accession: S72664

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140, 'C', 142-374 <KH2>

A;Cross-references: EMBL:X81695

C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 54.7%; Score 1225; DB 2; Length 374;

Best Local Similarity 96.6%; Pred. No. 2.8e-67;

Matches 225; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 168 SESTQKVDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEV 227

DB 141 SSBPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEV 200

QY 228 KFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 287

DB 201 KFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 260

Query Match	51.5%	Score 1154.5	DB 2	Length 377
Best Local Similarity	67.1%	Pred. No. 5.3e-63		
Matches 228	Conservative	19	Mismatches 32	Indels 61
				Gaps 7

Query Match	51.5%	Score 1152.5	DB 2	Length 377
Best Local Similarity	67.1%	Pred. No. 7e-63		
Matches 228	Conservative 19	Mismatches 32	Indels 61	Gaps 7
Qy	76	CNRTHNRVCECKEGRYLBIEF-----CLKHRSC---PPGFGVVOAGTPERNVTC	121	
Db	83	CNVNH-KPSNTKVDKRVELKTPGLDTHHTCPRCPEPKSCDTPPP-----C	126	
Qy	122	KRCPDGFNSNETSSKAP-CRRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDTHTC	180	
Db	127	PRCPEP-KSCDTPPPCPCRPBKSC-----DTPPPC	156	
Qy	181	PPCPAPELLGGPSVFLFPFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	240	
Db	157	PRCPAPELLGGPSVFLFPFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	216	
Qy	241	AKTKPREEQYNSTYRVVSVLTVLHODWNLNGKEYCKVSNKALPAPIEKTISKAKGQPREP	300	
Db	217	AKTKPREEQYNSTFRVSVLTVLHODWNLNGKEYCKVSNKALPAPIEKTISKAKGQPREP	276	
Qy	301	QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPTPVLDSGSGFFL	360	
Db	277	QVYTLPPSRBMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPTPVLDSGSGFFL	336	

Qy 361 YSKLTVDKSPWQQGVFSCSVNHEALHNHYTKQLSLSPG 400
||:|||||:|||||:|||||:|||||:
Db 337 YSRLTYDKSWOEGNVFSCSVNHEALHNRRTKQLSLSPG 376

RESULT 7

G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C>Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; E
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein T11
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:1133060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:6964124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (co light chain) #status experimental
F:27-83,140-200,245-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

51.3%; Score 1148.5; DB 1; Length 326;

Best Local Similarity 90.3%; Pred. No. 1.1e-62;

Matches 214; Conservative 8; Mismatches 8; Indels 7; Gaps 2;

170 STOKVDKT-----HTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHE 223

90 SNTKVDKTVKRCCKVECPAPP-VAGFSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHE 148

224 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVTLQHDWLNKGKEYCKVSNKALP 283

149 DPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVTLQHDWLNKGKEYCKVSNKGLP 208

284 APIETKISKAKQPPPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 343

209 APIETKISKAKQPPPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 268

344 NYKTTTPVLDSDGSPFLYSKLTVDKSRWQQGVFSCSVNHEALHNHYTQKSLSLSPG 400

269 NYKTTTPVLDSDGSPFLYSKLTVDKSRWQQGVFSCSVNHEALHNHYTQKSLSLSPG 325

RESULT 8

G2HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C>Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004

C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A:Cross-references: UNIPROT:P01861

A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant re

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30; 81-326 <PIN>

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,141-201,247-305/Disulfide bonds: #status predicted

F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

50.7%; Score 1136; DB 1; Length 327;

Best Local Similarity 89.5%; Pred. No. 6.1e-62;

Matches 212; Conservative 8; Mismatches 11; Indels 6; Gaps 1;

170 STOKVDKT-----HTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHE 223

90 SNTKVDKRVESKYGPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHE 149

224 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVTLQHDWLNKGKEYCKVSNKALP 283

150 DPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVTLQHDWLNKGKEYCKVSNKGLP 209

Qy 284 APIEKTISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSPDIAVEWESNGOPEN 343
:
Db 210 SSIKTIISKAGQPREPQVYTLPPSEMTKNQVSLTCLVKGFYPSPDIAVEWESNGOPEN 269

Qy 344 NYKITPPVLDSGSGFFLYSKLTVDKSRWQGNFVCSVMHEALHNHYTKLSLSPG 400
|||
Db 270 NYKITPPVLDSGSGFFLYSKLTVDKSRWQGNFVCSVMHEALHNHYTKLSLSPG 326

RESULT 9
G3HUMI
Ig gamma-3 heavy chain disease proteins - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A92219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain disease protein WIS
A;Reference number: A90442; MUID:81021548; PMID:6774747
A;Contents: heavy chain disease protein WIS
A;Accession: A90442
A;Molecule type: protein
A;Residues: 1-289 <PRA>
A;Note: The molecule is a dimer linked by 12 disulfide bonds: it has an extra interchain bond between residues 125 and 126. This bond is not present in the reference sequence.
A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 of the V region is taken from the reference that follows
R;Michaelson, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication of the hinge region.
A;Reference number: A92219; MUID:77118561; PMID:402363
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein WIS
A;Accession: A92219
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: The hinge region in gamma-3 chains is about four times as long as in other gammaglobulin segments (12-28)
R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the amino acid sequence of "heavy chain disease" protein ZUC.
A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues 12-97 of protein WIS
A;Accession: A90198
A;Molecule type: protein
A;Residues: 53-125, 'EE', 128-226, 228-289 <WOL>
A;Note: This protein lacks most of the V region, all of the CH1 region, and part of the R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.A.; Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deletion
A;Reference number: A93915; MUID:82247835; PMID:6808505
A;Contents: heavy chain disease protein Omn
A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157
A;Note: a carboxyl-terminal lysine is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6.140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 50.6%; Score 1133.5; DB 1; Length 289;
Best Local Similarity 70.8%; Pred.No. 7.6e-62;
Matches 218; Conservative 19; Mismatches 22; Indels 49; Gaps 5;

Qy 97 CLKHRSC---PPGGVVGVQAGTPERTVCKRPDGFFSNETSSKAP-CRKHTNCSVFOLL 152

F:20-82/Domain: immunoglobulin homology <IM1>
F:130-199/Domain: immunoglobulin homology <IM2>
F:236-303/Domain: immunoglobulin homology <IM3>
F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 41.2%; Score 923; DB 1; Length 323;
Best Local Similarity 61.5%; Pred. No. 4.8e-49;
Matches 177; Conservative 33; Mismatches 46; Indels 32; Gaps 5;
QY 123 RCPDGFSS-----NETSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGSESTQKVDKT 177
DB 57 RQSSGLYSLSVSVTSQQP-----VTCNV-----AHPATNTKVDKT 94
QY 178 ---HTC---PPCAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY 232
DB 95 VAPSTCSKPTCPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSDQDDPEVQFTWY 154
QY 233 YDGVVEVNAKTPREEQNSTYRVSVLTVLHQLDNLGKYEKCKVSKNKPAPIEKTIK 291
DB 155 INNEQVTAAPPLREQNFNSTIRVSVLPIHQDNLGKYEKCKVSKNKPAPIEKTIK 214
QY 293 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEFESNQGNPNYKTTTPVL 352
DB 215 ARGQPLEPKVYTMGPPEELSSRSVSLTCMNGFYPSDISVEKNGKAEKDNKTTPAVL 274
QY 353 DSDGSFFLYSLKLVDRKRWQGNVFCSCVMHEALHNHYTKSLSLSPG 400
DB 275 DSDGSFYLKSLVPTSEWQSGDVFCTCVNHEALHNHYTKSLSRSPG 322

RESULT 11

I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126
C:Genetics:
A:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IM>

Query Match 41.0%; Score 917.5; DB 2; Length 328;
Best Local Similarity 60.5%; Pred. No. 1.1e-48;
Matches 176; Conservative 35; Mismatches 43; Indels 37; Gaps 6;
QY 125 PDGFFNETSSKAPC----RKHTNCSVFGLLLTQKGNATHDNCISGSESTQKVDK--T 177
DB 59 PSLGLYSLSMVTVPASSLSKSYTCNV-----NHPATTTKVDKRVGT 100
QY 178 HTCPCCP-----APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 231
DB 101 KTKPPCPCIPACESP----GPSVFIFPPPKPKDTLMISRTPEVTCVVDVSDQENPEVQFSW 156
QY 232 YDGVVEVNAKTPREEQNSTYRVSVLTVLHQLDNLGKYEKCKVSKNKPAPIEKTIK 291
DB 157 YDGVVEVHTAQTRPKEQNSTYRVSVLPIHQDNLGKYEKCKVSKNKPAPITRIIS 216
QY 292 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEFESNQ--PENNYKTTTP 349
DB 217 KAKGQTRPQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEWQGNQPEPGEYRTTP 276
QY 350 PVLDSGGSFFLYSLKLVDRKRWQGNVFCSCVMHEALHNHYTKSLSLSPG 400
DB 277 PQDDVDGTYFLYSLKSVFSDKASWQGGIFQCAVMHEALHNHYTKSLSKTPG 327

RESULT 12

I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IM>

Query Match 41.0%; Score 917.5; DB 2; Length 328;
Best Local Similarity 60.5%; Pred. No. 1.1e-48;
Matches 176; Conservative 35; Mismatches 43; Indels 37; Gaps 6;
QY 125 PDGFFNETSSKAPC----RKHTNCSVFGLLLTQKGNATHDNCISGSESTQKVDK--T 177
DB 59 PSLGLYSLSMVTVPASSLSKSYTCNV-----NHPATTTKVDKRVGT 100
QY 178 HTCPCCP-----APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 231
DB 101 KTKPPCPCIPACESP----GPSVFIFPPPKPKDTLMISRTPEVTCVVDVSDQENPEVQFSW 156
QY 232 YDGVVEVNAKTPREEQNSTYRVSVLTVLHQLDNLGKYEKCKVSKNKPAPIEKTIK 291
DB 157 YDGVVEVHTAQTRPKEQNSTYRVSVLPIHQDNLGKYEKCKVSKNKPAPITRIIS 216
QY 292 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEFESNQ--PENNYKTTTP 349
DB 217 KAKGQTRPQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEWQGNQPEPGEYRTTP 276
QY 350 PVLDSGGSFFLYSLKLVDRKRWQGNVFCSCVMHEALHNHYTKSLSLSPG 400
DB 277 PQDDVDGTYFLYSLKSVFSDKASWQGGIFQCAVMHEALHNHYTKSLSKTPG 327

RESULT 13

I47162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:G433129; PIDN:AAA52220.1; PID:G433130
C:Genetics:
A:Gene: IgG4
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IM>

Query Match 40.9%; Score 915.5; DB 2; Length 277;
Best Local Similarity 61.3%; Pred. No. 1.2e-48;
Matches 176; Conservative 34; Mismatches 48; Indels 29; Gaps 6;
QY 125 PDGFFNETSSKAPC----RKHTNCSVFGLLLTQKGNATHDNCISGSESTQKVDK--T 177

Db 280 DVDGTFYSLAYDKARWDHGDKFECAMHEALHNNHYTKSISKTQG 327

Search completed: March 8, 2005, 14:46:13
Job time : 18.3022 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:56 ; Search time 73.9563 Seconds
(without alignments)
2769.633 Million cell updates/sec

Title: US-09-389-782A-5

Perfect score: 2240

Sequence: 1 ETPPPKLYHDETSQHLIC.....VMHEALNHYTKSLSPG 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1234	55.1	330	1	GC1_HUMAN	P01857 homo sapien
2	1234	55.1	465	2	Q6GMX6	Q6gmxx6 homo sapien
3	1234	55.1	466	2	Q6IN78	Q6in78 homo sapien
4	1234	55.1	469	2	Q7Z7P5	Q7z7p5 homo sapien
5	1234	55.1	470	2	Q6PJA4	Q6pj44 homo sapien
6	1234	55.1	470	2	Q7Z5W1	Q7z5w1 homo sapien
7	1234	55.1	472	2	Q6N089	Q6n089 homo sapien
8	1234	55.1	475	2	Q6GMW7	Q6gmw7 homo sapien
9	1234	55.1	476	2	Q6GMX1	Q6gmxx1 homo sapien
10	1230	54.9	473	2	Q6P055	Q6p055 homo sapien
11	1230	54.9	475	2	Q6M2Q6	Q6m2q6 homo sapien
12	1230	54.9	480	2	Q6N094	Q6n094 homo sapien
13	1230	54.9	481	2	Q6N097	Q6n097 homo sapien
14	1230	54.9	482	2	Q7Z351	Q7z351 homo sapien
15	1230	54.9	679	2	Q96PQ8	Q96pq8 homo sapien
16	1228	54.8	348	2	Q6PXX1	Q6pxx1 homo sapien
17	1228	54.8	473	2	Q6M2V7	Q6m2v7 homo sapien
18	1228	54.8	478	2	Q6P181	Q6p181 homo sapien
19	1228	54.8	480	2	Q6P0F1	Q6pf01 homo sapien
20	1228	54.8	544	2	Q6PJ95	Q6pj95 homo sapien
21	1227	54.8	466	2	Q6N096	Q6n096 homo sapien
22	1223	54.6	475	2	Q6N095	Q6n095 homo sapien
23	1212	54.1	487	2	Q652L2	Q652l2 mus sp. fv/
24	1154.5	51.5	354	2	Q86T72	Q86tt2 homo sapien
25	1150.5	51.4	521	2	Q8N4Y9	Q8n4y9 homo sapien
26	1149.5	51.3	518	2	Q6N030	Q6n030 homo sapien
27	1148.5	51.3	326	1	GC2_HUMAN	P01859 homo sapien
28	1148.5	51.3	417	2	Q6N093	Q6n093 homo sapien
29	1148	51.2	464	2	Q6MZU6	Q6mzu6 homo sapien
30	1144.5	51.1	509	2	Q8NF17	Q8nff7 homo sapien
31	1143.5	51.0	465	2	Q6P6C4	Q6p6c4 homo sapien

32	1136	50.7	327	1	GC4_HUMAN	P01861 homo sapien
33	1136	50.7	473	2	Q8T6C3	Q8t6c3 homo sapien
34	1134.5	50.6	493	2	Q68CN4	Q68cn4 homo sapien
35	1133.5	50.6	290	1	GC3_HUMAN	P01860 homo sapien
36	1127	50.3	476	2	Q6MZX7	Q6mzx7 homo sapien
37	1013	45.2	401	1	T11B_HUMAN	O00300 homo sapien
38	923	41.2	323	1	GC_RABIT	P01870 oryctolagus
39	918	41.0	337	2	Q95M34	Q95m34 equus cabal
40	904.5	40.4	329	1	GC3_CAVPO	Q06112 cavia porce
41	897.5	40.1	401	2	Q6P112	Q6p112 mus musculu
42	893.5	39.9	401	1	T11B_MOUSE	O08712 mus musculu
43	877	39.2	401	1	T11B_RAT	O08727 rattus norv
44	850	37.9	470	2	Q7TMK1	Q7tmk1 mus musculu
45	847.5	37.8	329	1	GC3_MOUSE	P22436 mus musculu

ALIGNMENTS

RESULT 1

GC1_HUMAN	STANDARD;	PRT;	330 AA.
ID GC1_HUMAN			
AC P01857;			
DT 21-JUL-1986 (Rel. 01, Created)			
DT 21-JUL-1986 (Rel. 01, Last sequence update)			
DT 25-OCT-2004 (Rel. 45, Last annotation update)			
DE Ig gamma-1 chain C region.			
GN Name=IGHG1;			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=82274238; PubMed=6287432;			
RA Ellison J.W., Berson B.J., Hood L.E.;			
RT "The nucleotide sequence of a human immunoglobulin C gamma gene."			
RL Nucleic Acids Res. 10:4071-4079 (1982).			
RN [2]			
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX MEDLINE=71064024; PubMed=5489771;			
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
Waxdal M.J., Edelman G.M.;			
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL Biochemistry 9:3161-3170 (1970).			
RN [3]			
RP SEQUENCE OF 136-329 (EU).			
RX MEDLINE=71064025; PubMed=5530842;			
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
Edelman G.M.;			
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL Biochemistry 9:3171-3181 (1970).			
RN [4]			
RP SEQUENCE (MYELOMA PROTEIN NIE).			
RX MEDLINE=77070269; PubMed=826475;			
RA Ponstingl H., Hilschmann N.;			
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."			
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).			
RN [5]			
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX MEDLINE=83289131; PubMed=6884994;			
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).			
RN [6]			
RP DISULFIDE BONDS.			
RX MEDLINE=71064027; PubMed=4923144;			

RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RL Intrachain disulfide bonds.";
 RN Biochemistry 9:3188-3196(1970).
 RP [7]
 RX DISULFIDE BONDS.
 RA MEDLINE=7707026; PubMed=1002129;
 RX Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie). I: purification and
 RT characterization of the protein, the L- and H-chains, the cyanogen
 RT bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RP [8]
 RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RA MEDLINE=81208100; PubMed=7236608;
 RX Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -1- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the
 CC GIM(3) marker and the GIM (non-1) markers.
 CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,
 CC 116, 198, 269 and 272.
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of
 CC residues 198, 267 and 272.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A93433; GHHU.
 DR PDB; 1AJ7; X-ray; H=1-103.
 DR PDB; 1DSB; X-ray; B/H=1-101.
 DR PDB; 1DS1; X-ray; H=1-101.
 DR PDB; 1D6V; X-ray; H=1-101.
 DR PDB; 1DN2; X-ray; A/B=120-326.
 DR PDB; 1E4K; X-ray; A/B=106-329.
 DR PDB; 1FC1; X-ray; A/B=106-329.
 DR PDB; 1FC2; X-ray; D=106-329.
 DR PDB; 1FCC; X-ray; A=121-326.
 DR PDB; 1H2H; X-ray; H/K=1-330.
 DR PDB; 1I7Z; X-ray; B/D=1-103.
 DR PDB; 1IIX; X-ray; A/B=107-330.
 DR PDB; 1L6X; X-ray; A/B=107-330.
 DR PDB; 1QX; X-ray; A=120-326.
 DR PDB; 1QX; X-ray; A/B=119-330.
 DR PDB; 2RCS; X-ray; H=1-103.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; P:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG; 3.
 DR PROSITE; PS0835; IG LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW 3D-structure; Direct protein sequencing; Glycoprotein;
 FT Immunoglobulin C region; Immunoglobulin domain.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 Hinge.

FT	DOMAIN	111	223	CH2.
FT	DOMAIN	224	330	CH3.
FT	DISULFID	27	83	
FT	DISULFID	103	103	
FT	DISULFID	109	109	Interchain (with light chain).
FT	DISULFID	112	112	Interchain (with heavy chain).
FT	DISULFID	144	204	Interchain (with heavy chain).
FT	DISULFID	250	308	
FT	CARBOHYD	180	180	
FT	VARIANT	97	97	
FT	VARIANT	239	239	N-linked (GlcNAc. .). K -> R (in GIM(3) marker). /FTID=VAR_003886. D -> E (in GIM(non-1) marker). /FTID=VAR_003887. L -> M (in GIM(non-1) marker). /FTID=VAR_003888.
FT	VARIANT	241	241	
FT	STRAND	23	24	
FT	STRAND	26	33	
FT	STRAND	38	38	
FT	STRAND	41	41	
FT	TURN	42	45	
FT	TURN	48	49	
FT	STRAND	50	52	
FT	STRAND	57	58	
FT	TURN	59	61	
FT	STRAND	62	71	
FT	HELIX	73	75	
FT	TURN	76	78	
FT	STRAND	82	87	
FT	TURN	88	91	
FT	STRAND	92	97	
FT	TURN	102	103	
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
FT	STRAND	141	149	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	167	
FT	STRAND	171	172	
FT	TURN	176	177	
FT	STRAND	179	180	
FT	STRAND	183	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	STRAND	261	266	
FT	TURN	267	268	
FT	STRAND	269	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	306	311	
FT	TURN	313	314	
FT	HELIX	316	318	
FT	STRAND	319	324	
SQ	SEQUENCE	330 AA;	36106 MW;	3770EE106C2FA33D CRC64;

Query Match 55.1%; Score 1234; DB 1; Length 330;
 Best Local Similarity 92.1%; Pred. No. 3.2e-73;
 Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;
 QY 159 THDNICS-----GNSESTQKV-----DKTHTCPCPAPELLGGPSVFLFPKPKDTLMIS 208
 Db 78 TQYICNVNHKPSNTKVDKKEPKSKCDKTHTCPPAPELLGGPSVFLFPKPKDTLMIS 137

QY 209 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 268
 DB 138 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 197
 QY 269 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 328
 DB 198 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 257
 QY 329 SDIAVESWGQPNENYKTTTPPVLDSGDSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHN 388
 DB 258 SDIAVESWGQPNENYKTTTPPVLDSGDSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHN 317
 QY 389 HYTKQSLSLSPG 400
 DB 318 HYTKQSLSLSPG 329

RESULT 2
 Q6GMX6 PRELIMINARY; PRT; 465 AA.

AC Q6GMX6
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

SEQUENCE FROM N.A.
 RP TISSUE=Primary B-Cells;
 RC MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

SEQUENCE FROM N.A.
 RP TISSUE=Primary B-Cells;
 RC Strausberg R.;
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073766; AA73766.1; -;
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig v.
 DR Pfam; PF07654; Cl-set; 3.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00409; IG1; 2.
 DR SMART; SM00407; IG1; 3.
 DR SMART; SM00406; IG1; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.

SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
 Query Match 55.1%; Score 1234; DB 2; Length 465;
 Best Local Similarity 92.1%; Pred. No. 4.7e-73;
 Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;
 QY 159 THDNICS-----GNSESTOKV-----DKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 208
 DB 213 TQYICNNVNHKPSNTKVDKKVPEKSCDKHTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 272
 QY 209 RIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 268
 DB 273 RIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 332
 QY 269 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 328
 DB 333 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 392
 QY 329 SDIAVESWGQPNENYKTTTPPVLDSGDSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHN 388
 DB 393 SDIAVESWGQPNENYKTTTPPVLDSGDSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHN 452
 QY 389 HYTKQSLSLSPG 400
 DB 453 HYTKQSLSLSPG 464

RESULT 3
 Q6IN78 PRELIMINARY; PRT; 466 AA.

AC Q6IN78
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

SEQUENCE FROM N.A.
 RP TISSUE=Peripheral Nervous System;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

SEQUENCE FROM N.A.
 RP TISSUE=Peripheral Nervous System;
 RC Strausberg R.;
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC072419; AA72419.1; -;
 DR HSSP; P01861; 1ADO.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2; 3.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCDE81076E CRC64;

Query Match 55.1%; Score 1234; DB 2; Length 466;
 Best Local Similarity 92.5%; Pred. No. 4.7e-73;
 Matches 233; Conservative 2; Mismatches 7; Indels 10; Gaps 2;

QY 159 THDNICSGNSE-STQKV-----DKHTCTCPCPAPPELLGGPSVFLPPKPKDTLMIS 208
 Db 214 TQYICNVNHPKNTKVDKKEVPEKSCDKHTCTCPCPAPPELLGGPSVFLPPKPKDTLMIS 273
 QY 209 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWL 268
 Db 274 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWL 333
 QY 269 NGKEYCKKSVNKPALPAIEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328
 Db 334 NGKEYCKKSVNKPALPAIEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 393
 QY 329 SDIAVWESNGQPNENYKTPPPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHN 388
 Db 394 SDIAVWESNGQPNENYKTPPPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHN 453
 QY 389 HYTKSLSLSPG 400
 Db 454 HYTKSLSLSPG 465

RESULT 4
 Q7Z7P5 PRELIMINARY; PRT; 469 AA.
 AC Q7Z7P5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE IGHG1 protein
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Udwin T.B., Toshuyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."; [2]
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC051328; AAHS1328.1; -
 DR HSSP; P01857; 1HZH.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 55.1%; Score 1234; DB 2; Length 469;
 Best Local Similarity 92.1%; Pred. No. 4.7e-73;
 Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;

QY 159 THDNICS-----GNSESTQKV-----DKHTCTCPCPAPPELLGGPSVFLPPKPKDTLMIS 208
 Db 217 TQYICNVNHPKNTKVDKKEVPEKSCDKHTCTCPCPAPPELLGGPSVFLPPKPKDTLMIS 276
 QY 209 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWL 268
 Db 277 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWL 336
 QY 269 NGKEYCKKSVNKPALPAIEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328
 Db 337 NGKEYCKKSVNKPALPAIEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 396
 QY 329 SDIAVWESNGQPNENYKTPPPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHN 388
 Db 397 SDIAVWESNGQPNENYKTPPPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHN 456
 QY 389 HYTKSLSLSPG 400
 Db 457 HYTKSLSLSPG 468

RESULT 5
 Q6PUJ4 PRELIMINARY; PRT; 470 AA.
 ID Q6PUJ4
 AC Q6PUJ4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Udwin T.B., Toshuyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."; [2]
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RC SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -;
DR HSP; P01861; IADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11PD7D99 CRC64;
Query Match 55.1%; Score 1234; DB 2; Length 470;
Best Local Similarity 92.1%; Pred. No. 4.8e-73;
Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;
QY 159 THDNICS-----GNSSTQKV-----DKTHTCPCPAPPELLGGPSVLPFPKPKDTLMIS 208
DB 218 TQTYICNVNHNKPSNTKVDKKVPEKSCDKTHTCPCPAPPELLGGPSVLPFPKPKDTLMIS 277
QY 209 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVWSVLTVLHQDWL 268
DB 278 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVWSVLTVLHQDWL 337
QY 269 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328
DB 338 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 397
QY 329 SDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN 388
DB 398 SDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN 457
QY 389 HYTKQSLSLSPG 400
DB 458 HYTKQSLSLSPG 469
RESULT 6
Q725W1 ID Q725W1 PRELIMINARY; PRT; 470 AA.
AC Q725W1
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RC SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -;
DR HSP; P01857; IHZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
Query Match 55.1%; Score 1234; DB 2; Length 470;
Best Local Similarity 92.1%; Pred. No. 4.8e-73;
Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;
QY 159 THDNICS-----GNSSTQKV-----DKTHTCPCPAPPELLGGPSVLPFPKPKDTLMIS 208
DB 218 TQTYICNVNHNKPSNTKVDKKVPEKSCDKTHTCPCPAPPELLGGPSVLPFPKPKDTLMIS 277
QY 209 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVWSVLTVLHQDWL 268
DB 278 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVWSVLTVLHQDWL 337
QY 269 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328
DB 338 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 397
QY 329 SDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN 388
DB 398 SDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN 457
QY 389 HYTKQSLSLSPG 400
DB 458 HYTKQSLSLSPG 469
RESULT 7
Q6N089 ID Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;

RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640627; CAE45781.1; -;
 DR HSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG.cl.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 55.1%; Score 1234; DB 2; Length 472;
 Best Local Similarity 92.5%; Pred. No. 4.8e-73;
 Matches 233; Conservative 2; Mismatches 7; Indels 10; Gaps 2;

QY 159 THDNICSGSE-STQKV-----DKHTCTCPAPPELLGGPSVFLPPKPKDTLMIS 208
 DB 220 TQTYICNVNHPSTKVDKRVKPSCKDHTCTCPAPPELLGGPSVFLPPKPKDTLMIS 279
 QY 209 RTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWL 268
 DB 280 RTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWL 339
 QY 269 NGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGYF 328
 DB 340 NGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGYF 399
 QY 329 SDIAVESNGQPNKYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVNHHEALHN 388
 DB 400 SDIAVESNGQPNKYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVNHHEALHN 459
 QY 389 HYTKSLSLSPG 400
 DB 460 HYTKSLSLSPG 471

RESULT 8
 Q6GMW7 PRELIMINARY; PRT; 475 AA.
 ID Q6GMW7
 AC Q6GMW7
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073782; AAH73782.1; -;
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG.cl.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 55.1%; Score 1234; DB 2; Length 475;
 Best Local Similarity 92.1%; Pred. No. 4.8e-73;
 Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;

QY 159 THDNICSGSE-STQKV-----DKHTCTCPAPPELLGGPSVFLPPKPKDTLMIS 208
 DB 223 TQTYICNVNHPSTKVDKRVKPSCKDHTCTCPAPPELLGGPSVFLPPKPKDTLMIS 282
 QY 209 RTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWL 268
 DB 283 RTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWL 342
 QY 269 NGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGYF 328
 DB 343 NGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGYF 402
 QY 329 SDIAVESNGQPNKYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVNHHEALHN 388
 DB 403 SDIAVESNGQPNKYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVNHHEALHN 462
 QY 389 HYTKSLSLSPG 400
 DB 463 HYTKSLSLSPG 474

RESULT 9
 Q6GMX1 PRELIMINARY; PRT; 476 AA.
 ID Q6GMX1
 AC Q6GMX1
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00407; IG1; 4.
DR SMART; SM00406; IG1; 3.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
Query Match 55.1%; Score 1234; DB 2; Length 476;
Best Local Similarity 92.1%; Pred. No. 4.8e-73;
Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;
Qy 159 THDNICS-----GNSESTQKV-----DKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 208
Db 224 TQYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 283
Qy 209 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 268
Db 284 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 343
Qy 269 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328
Db 344 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 403
Qy 329 SDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQOQGNVFSCSVMEALHN 388
Db 404 SDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQOQGNVFSCSVMEALHN 463
Qy 389 HYTKSLSLSPG 400
Db 464 HYTKSLSLSPG 475
RESULT 10
Q6P055 PRELIMINARY; PRT; 473 AA.
AC Q6P055
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Mullahy S.J.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -;
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG1; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;
Query Match 54.9%; Score 1230; DB 2; Length 473;
Best Local Similarity 91.7%; Pred. No. 8.8e-73;
Matches 231; Conservative 4; Mismatches 7; Indels 10; Gaps 2;
Qy 159 THDNICS-----GNSESTQKV-----DKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 208
Db 221 TQYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 280
Qy 209 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 268
Db 281 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 340
Qy 269 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328
Db 341 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 400
Qy 329 SDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQOQGNVFSCSVMEALHN 388
Db 401 SDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQOQGNVFSCSVMEALHN 460
Qy 389 HYTKSLSLSPG 400
Db 461 HYTKSLSLSPG 472
RESULT 11
Q6WZQ6

DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
DR PROSITE; PS02040; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;

Query Match 54.9%; Score 1230; DB 2; Length 679;
Best Local Similarity 97.4%; Pred. No. 1.3e-72;
Matches 227; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 168 SESTQKVDKTHTCPPCPAPBLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 227
Db : |||||
446 SAEPKSCDKHTCCPPCPAPBLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 505
|||
QY 228 KFNWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 287
Db |||||
506 KFNWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 565
|||
QY 288 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 347
Db |||||
566 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 625
|||
QY 348 TTPVLDSDGSGFFLYSKLTVDKSRWQQGNVPCSWMEALHNHYTQKSLSLSPG 400
Db |||||
626 TTPVLDSDGSGFFLYSKLTVDKSRWQQGNVPCSWMEALHNHYTQKSLSLSPG 678
|||

Search completed: March 8, 2005, 14:44:38
Job time : 75.9563 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:11 ; Search time 85.1551 Seconds
(without alignments)
1843.986 Million cell updates/sec

Title: US-09-389-782A-6
Perfect score: 2274
Sequence: 1 ETPPKYLHDETSQLLC.....VMHEALHNHYTKSLSPG 406

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2274	100.0	406	4 AAB80902	Aab80902 Human OPG
2	2274	100.0	406	4 AAY72920	Aay72920 Human OPG
3	2256.5	99.2	413	4 AAB80900	Aab80900 Human OPG
4	2256.5	99.2	413	4 AAY72918	Aay72918 Human ost
5	2227	97.9	400	4 AAB80901	Aab80901 Human OPG
6	2227	97.9	400	4 AAY72919	Aay72919 Human OPG
7	2227	97.9	422	4 AAB66993	Aab66993 OPG-FC. 4
8	2226	97.9	425	5 ABG71831	Abg71831 Human OPG
9	2224.5	97.8	407	4 AAB80899	Aab80899 Human OPG
10	2224.5	97.8	407	4 AAY72917	Aay72917 Human ost
11	2191	96.4	404	4 AAB80903	Aab80903 Human OPG
12	2191	96.4	404	4 AAY72921	Aay72921 Human OPG
13	1521.5	66.9	659	6 ABJ37103	Abj37103 Concatame
14	1521.5	66.9	659	8 ADQ79910	Adq79910 Human tum
15	1516	66.7	489	8 ADM32913	Adm32913 Amino aci
16	1513.5	66.6	490	6 ABJ37099	Abj37099 Concatame
17	1513.5	66.6	490	8 ADQ79902	Adq79902 Human tum
18	1513.5	66.6	720	6 ABJ37101	Abj37101 Concatame
19	1513.5	66.6	720	8 ADQ79906	Adq79906 Human tum
20	1501	66.0	518	4 AAB50080	Aab50080 TNFR. Fc f
21	1501	66.0	518	4 AAB70001	Aab70001 sTNFR (075
22	1490	65.5	485	2 AAR24016	Aar24016 Fusion pr
23	1487.5	65.4	450	7 ADL06639	Adl06639 sTNFR.II
24	1487	65.4	518	2 AAR51003	Aar51003 Sequence
25	1470.5	64.7	444	5 ABG71833	Abg71833 RANK bind

26	1468.5	64.6	440	7 ADJ66000	Adj66000 Herpes vi
27	1468.5	64.6	440	8 ADP03589	Adp03589 Infection
28	1460	64.2	439	8 ADO47876	Ado47876 Alpha-Her
29	1458.5	64.1	443	6 ABP58181	Abp58181 Human RAN
30	1458.5	64.1	443	6 AAE34361	Aae34361 Human RAN
31	1421	62.5	443	7 ADB17000	Adb17000 Murine RA
32	1419.5	62.4	442	7 ADB17001	Adb17001 Human RAN
33	1419.5	62.4	443	7 ADB17002	Adb17002 Human RAN
34	1389.5	61.1	608	6 ABJ37102	Abj37102 Concatame
35	1389.5	61.1	608	8 ADQ79908	Adq79908 Human tum
36	1381.5	60.8	444	6 ABJ37098	Abj37098 Concatame
37	1381.5	60.8	444	8 ADQ79900	Adq79900 Human tum
38	1381.5	60.8	628	6 ABJ37100	Abj37100 Concatame
39	1381.5	60.8	628	8 ADQ79904	Adq79904 Human tum
40	1349	59.3	376	2 AAW60037	Aaw60037 Antigenic
41	1348.5	59.3	396	8 ADF57557	Adf57557 Mouse ymk
42	1339.5	58.9	445	7 ADL06637	Adl06637 sTNFR.Ig
43	1338.5	58.9	398	7 ABW02717	Abw02717 Mouse tms
44	1338.5	58.9	398	8 ADJ45758	Adj45758 Murine tm
45	1334	58.7	376	2 AAW50287	Aaw50287 Human Fas

ALIGNMENTS

RESULT 1
AAB80902
ID AAB80902 standard; protein; 406: AA.

XX AAB80902;
XX
XX 31-MAY-2001 (first entry)
XX
XX Human OPG(22-201)-FcdeltaC fusion protein.
XX
XX Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
XX multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
XX osteoclast formation inhibition; bone resorption inhibition;
XX immunoglobulin.
XX Homo sapiens.
XX
XX WO200117543-A2.
XX
XX 15-MAR-2001.
XX
XX 18-AUG-2000; 2000WO-US022806.
XX
XX 03-SEP-1999; 99US-00389545.
XX (AMGE-) AMGEN INC.
XX Dunstan CR;
XX
XX WPI; 2001-265936/27.
XX
XX Preventing or treating lytic bone diseases, particularly associated with
XX cancer or metastasis, by administering an osteoprotegrin polypeptide.
XX
XX Disclosure; Fig 6; 87pp; English.

The present invention relates to a method for the prevention or treatment of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypeptide or OPG fusion protein. The present sequence is one such OPG fusion protein. OPG inhibits formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The OPG polypeptide can be used in a method of preventing or treating lytic bone disease, for preventing metastasis of cancer to bone (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal, rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal tract, multiple myeloma or lymphoma) and preventing the osteosclerotic

CC bone metastasis. The OPG fusion polypeptides are used in the prevention
 CC or treatment of loss of bone mass, which occurs in conditions including
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
 CC congenital forms of osteoporosis (osteogenesis imperfecta,
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
 CC hyperthyroidism and renal function disorders; osteopaenia following
 CC surgery, induced by steroid administration, and associated with disorders
 CC of the small and large intestine and with chronic hepatic and renal
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
 CC are also used in the replacement of structurally sound bone with
 CC in adults and juveniles; hyperparathyroidism, in congenital bone
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone
 CC metastases. The OPG fusion proteins can exhibit increased circulating
 CC half-lives and slower clearance times, thereby providing a more sustained
 CC activity. The OPG fusion protein comprises a fragment of the human OP
 CC protein and the Fc region of immunoglobulin IgGammal (the hinge, CH2 and
 CC CH3 regions; see AAB80897-8)

XX SQ Sequence 406 AA;

Query Match 100.0%; Score 2274; DB 4; Length 406;
 Best Local Similarity 100.0%; Pred. No. 6.4e-131;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHTAKWKTCAPCPDHYTDSWHTSDECL 60
 DB 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHTAKWKTCAPCPDHYTDSWHTSDECL 60

QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 120
 DB 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 120

QY 121 CKRCPGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSETQKCGIDVT 180
 DB 121 CKRCPGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSETQKCGIDVT 180

QY 181 DKHTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 240
 DB 181 DKHTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 240

QY 241 GVEVHNKTPREEQVNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIETISKAK 300
 DB 241 GVEVHNKTPREEQVNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIETISKAK 300

QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGYIPSDIAVWESNGQPENNYKTTPPVLDS 360
 DB 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGYIPSDIAVWESNGQPENNYKTTPPVLDS 360

QY 361 DGSFFLYSKLTVDKSRWQQGNVFCFVSVWHEALHNHYTQKSLSLSPG 406
 DB 361 DGSFFLYSKLTVDKSRWQQGNVFCFVSVWHEALHNHYTQKSLSLSPG 406

RESULT 2

AA72920
 ID AAY72920 standard; protein; 406 AA.
 XX
 AC AAY72920;
 XX
 DT 13-JUN-2001 (first entry)
 XX
 DE Human OPG (22-201 aa)-Fc region (lacking 1-5 residues) fusion protein.

XX KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
 KW periodontal.
 XX OS Homo sapiens.
 XX FH Key
 FT Region Location/Qualifiers
 FT 1.179 /note= "Derived from human osteoprotegerin fragment (22-
 FT 201 residues)"
 FT Region 180 /label= Linker
 FT Region 181.406
 FT /note= Human IgG1 Fc region lacking 1-5 residues;
 FT (Corresponds to 6-231 residues of IgG1 Fc region)
 XX W0200118203-A1.
 PD 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-US022797.
 PF 03-SEP-1999; 99US-00389782.
 PR (AMGE-) AMGEN INC.
 PA Dunstan CR, Wooden SK, Mann MB;
 PI WPI; 2001-244572/25.
 DR Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
 XX by e.g. osteoporosis, Paget's disease and osteomyelitis.
 PT Claim 7; Fig 6; 119pp; English.
 PS The present sequence is a fusion protein comprising a sequence derived
 CC from human osteoprotegerin (OPG; 22-201 residues) which is fused with
 CC human immunoglobulin G1 (IgG1) Fc region lacking 1-5 residues, by a
 CC linker. OPG negatively regulates the formation of osteoclasts in vitro
 CC and in vivo. It blocks the differentiation of osteoclasts from monocyte
 CC or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion
 CC protein is administered for the treatment of bone loss resulting from
 CC osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia
 CC associated with surgery or steroid administration, osteonecrosis, bone
 CC loss due to rheumatoid arthritis, periodontal bone loss, osteolytic
 CC metastasis and/or prosthetic loosening

XX SQ Sequence 406 AA;

Query Match 100.0%; Score 2274; DB 4; Length 406;
 Best Local Similarity 100.0%; Pred. No. 6.4e-131;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHTAKWKTCAPCPDHYTDSWHTSDECL 60
 DB 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHTAKWKTCAPCPDHYTDSWHTSDECL 60

QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 120
 DB 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 120

QY 121 CKRCPGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSETQKCGIDVT 180
 DB 121 CKRCPGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSETQKCGIDVT 180

QY 181 DKHTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 240
 DB 181 DKHTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 240

QY 241 GVEVHNKTPREEQVNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIETISKAK 300

Db 241 GVEVHNKTPREQYNTYTRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKTSKAK 300
Qy 301 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLD 360
Db 301 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLD 360
Qy 361 DGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 406
Db 361 DGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 406

RESULT 3
AAB80900
ID AAB80900 standard; protein; 413 AA.

XX AC AAB80900;
XX DT 31-MAY-2001 (first entry)
XX DE Human OPG(22-201)-Fc fusion protein.
XX Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegerin;
KW osteoclast formation inhibition; bone resorption inhibition;
KW immunoglobulin.
XX OS Homo sapiens.
XX PN W0200117543-A2.
XX PD 15-MAR-2001.
XX PF 18-AUG-2000; 2000WO-US022806.
XX PR 03-SEP-1999; 99US-00389545.
XX PA (AMGE-) AMGEN INC.
XX PI Dunstan CR;
XX PS WPI; 2001-265936/27.
XX Preventing or treating lytic bone diseases, particularly associated with
XX cancer or metastasis, by administering an osteoprotegerin polypeptide.
XX Disclosure; Fig 4; 87pp; English.

CC The present invention relates to a method for the prevention or treatment
CC of lytic bone disease or multiple myeloma. Also the method can be used
CC for preventing metastasis of cancer to bone or osteosclerotic bone
CC metastasis. The method comprises administering an OPG (osteoprotegerin)
CC polypeptide or OPG fusion protein. The present sequence is one such OPG
CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone
CC resorption) by blocking differentiation from monocytes/macrophage
CC precursors. The OPG polypeptide can be used in a method of preventing or
CC treating lytic bone disease, for preventing metastasis of cancer to bone
CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic
CC bone metastasis. The OPG fusion polypeptides are used in the prevention
CC or treatment of loss of bone mass, which occurs in conditions including
CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
CC congenital forms of osteoporosis (osteogenesis imperfecta,
CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
CC due to immobilisation of extremities; Paget's disease of bone (osteitis
CC deformans) in adults and juveniles; osteomyelitis, or an infectious
CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
CC hyperthyroidism and renal function disorders; osteopaenia following
CC surgery, induced by steroid administration, and associated with disorders

CC of the small and large intestine and with chronic hepatic and renal
CC diseases; osteonecrosis, or bone cell death, associated with traumatic
CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
CC cell anaemia, systemic lupus erythematosus and other conditions; bone
CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
CC are also used in the replacement of structurally sound bone with
CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
CC in adults and juveniles; hyperparathyroidism, in congenital bone
CC disorders such as fibrous dysplasia, and in osteosclerotic bone
CC metastases. The OPG fusion proteins can exhibit increased circulating
CC half-lives and slower clearance times, thereby providing a more sustained
CC activity. The OPG fusion protein comprises a fragment of the human OPG
CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and
CC CH3 regions; see AAB80897-8)
XX
SQ Sequence 413 AA;

Query Match 99.2%; Score 2256.5; DB 4; Length 413;
Best Local Similarity 98.1%; Pred. NO. 7.7e-130;
Matches 405; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

Qy 1 ETPPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWTVCAPCPDHYTDSWHTSDECL 60
Db 1 ETPPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWTVCAPCPDHYTDSWHTSDECL 60
Qy 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLIEFCLKHRSCPPGFGVVQAGTPERTV 120
Db 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLIEFCLKHRSCPPGFGVVQAGTPERTV 120
Qy 121 CKRCPDGPFNSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 180
Db 121 CKRCPDGPFNSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 180
Qy 181 -----DKTHTCPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 233
Db 181 AAEPKSCDKTHCTCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 240
Qy 234 KFNWYVDGVEVHNKATKPREEQYNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIE 293
Db 241 KFNWYVDGVEVHNKATKPREEQYNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIE 300
Qy 294 KITSKAGQPREQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKT 353
Db 301 KITSKAGQPREQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKT 360
Qy 354 TTPVLDSGDSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 406
Db 361 TTPVLDSGDSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 413

RESULT 4
AA72918
ID AA72918 standard; protein; 413 AA.

XX AC AA72918;
XX DT 13-JUN-2001 (first entry)
XX Human osteoprotegerin (22-201 residues)-IgG1 Fc region fusion protein.
XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
KW periodontal.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX Key 1..179
XX Region /note= "Derived from human osteoprotegerin fragment (22-
XX 201 residues)"

```

FT Region 180..182
FT /label= Linker
FT Region 183..413
FT /label= Human_IgG1_Fc_region
PN WO200118203-A1.
XX 15-MAR-2001.
XX
XX 18-AUG-2000; 2000WO-US022797.
XX
XX 03-SEP-1999; 99US-00389782.
XX
XX (AMGE-) AMGEN INC.
XX
XX Dunstan CR, Wooden SK, Mann MB;
XX WPI; 2001-244572/25.
XX
XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
XX by e.g. osteoporosis, Paget's disease and osteomyelitis.
XX
XX Example 1; Fig 4; 119pp; English.
XX
XX The present sequence is a fusion protein comprising a sequence derived
XX from human osteoprotegerin (OPG; 22-201 residues) which is fused with
XX human immunoglobulin G1 (IgG1) Fc region by a linker. OPG negatively
XX regulates the formation of osteoclasts in vitro and in vivo. It blocks
XX the differentiation of osteoclasts from monocyte or macrophage precursors
XX and the reabsorption of bone. The OPG-Fc fusion protein is administered
XX for the treatment of bone loss resulting from osteoporosis, Paget's
XX disease, osteomyelitis, hypercalcaemia, osteopenia associated with
XX surgery or steroid administration, osteonecrosis, bone loss due to
XX rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or
XX prosthetic loosening
XX
XX SQ Sequence 413 AA;
XX
XX Query Match 99.2%; Score 2256.5; DB 4; Length 413;
XX Best Local Similarity 98.1%; Pred. No. 7.7e-130;
XX Matches 405; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
XX
QY 1 ETEPPKYLHYDETSQLLCDKCPPTGYLKHQCTAKWTVCAPCPDHYHYTDSWHTSDECL 60
DB 1 ETEPPKYLHYDETSQLLCDKCPPTGYLKHQCTAKWTVCAPCPDHYHYTDSWHTSDECL 60
QY 61 YCSPVKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKXHSRCPGFGVVGAGTPERNTV 120
DB 61 YCSPVKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKXHSRCPGFGVVGAGTPERNTV 120
QY 121 CKRCPDGFSTNETSSKAPCRKHTNCVSFGLLLTKGNATHDNCNSGSESTQKCGIDVTV 180
DB 121 CKRCPDGFSTNETSSKAPCRKHTNCVSFGLLLTKGNATHDNCNSGSESTQKCGIDVTV 180
QY 181 -----DKTHTCPCPAPELLGGPSVFLFPKPKDITLMSITPVTVCVVDVSHEDREV 233
DB 181 AAEPKSCDTHTCPPAPELLGGPSVFLFPKPKDITLMSITPVTVCVVDVSHEDREV 240
QY 234 KFNWYVDGVEVHNATKPREQVNSTYRVSVVLTVLHQDLWLGKCYKCKVSNKALPAPIE 293
DB 241 KFNWYVDGVEVHNATKPREQVNSTYRVSVVLTVLHQDLWLGKCYKCKVSNKALPAPIE 300
QY 294 KTIISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNQPPENNYKT 353
DB 301 KTIISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNQPPENNYKT 360
QY 354 TTPVLDSGSPFLYSLKLTVDKSRWQGNVFCVSNVMEALHNHYTKLSLSLSPG 406
DB 361 TTPVLDSGSPFLYSLKLTVDKSRWQGNVFCVSNVMEALHNHYTKLSLSLSPG 413

```

RESULT 5
AAB80901

ID AAB80901 standard; protein; 400 AA.
 XX
 AC AAB80901;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human OPG(22-194)-FcdeltaC fusion protein.
 XX
 KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
 KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
 KW osteoclast formation inhibition; bone resorption inhibition;
 KW immunoglobulin.
 XX
 OS Homo sapiens.
 XX
 PN WO200117543-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-US022806.
 XX
 PR 03-SEP-1999; 99US-00389545.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 PI Dunstan CR;
 XX
 DR WPI; 2001-265936/27.
 XX
 XX Preventing or treating lytic bone diseases, particularly associated with
 XX cancer or metastasis, by administering an osteoprotegrin polypeptide.
 XX
 PS Claim 11; Fig 5; 87pp; English.
 XX
 CC The present invention relates to a method for the prevention or treatment
 CC of lytic bone disease or multiple myeloma. Also the method can be used
 CC for preventing metastasis of cancer to bone or osteosclerotic bone
 CC metastasis. The method comprises administering an OPG (osteoprotegrin)
 CC polypeptide or OPG fusion protein. The present sequence is one such OPG
 CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone
 CC resorption) by blocking differentiation from monocytes/macrophage
 CC precursors. The OPG polypeptide can be used in a method of preventing or
 CC treating lytic bone disease, for preventing metastasis of cancer to bone
 CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
 CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
 CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic
 CC bone metastasis. The OPG fusion polypeptides are used in the prevention
 CC or treatment of loss of bone mass, which occurs in conditions including
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
 CC congenital forms of osteoporosis (osteogenesis imperfecta,
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
 CC hyperthyroidism and renal function disorders; osteopaenia following
 CC surgery, induced by steroid administration, and associated with disorders
 CC of the small and large intestine and with chronic hepatic and renal
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
 CC are also used in the replacement of structurally sound bone with
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
 CC in adults and juveniles; hyperparathyroidism, in congenital bone
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone
 CC metastases. The OPG fusion proteins can exhibit increased circulating
 CC half-lives and slower clearance times, thereby providing a more sustained
 CC activity. The OPG fusion protein comprises a fragment of the human OPG
 CC protein and the Fc region of immunoglobulin IgGammal (the hinge, CH2 and

```

CC CH3 regions; see AAB80897-8)
XX Sequence 400 AA;
SQ

Query Match          97.9%; Score 2227; DB 4; Length 400;
Best Local Similarity 98.5%; Pred. No. 4.7e-128;
Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKHCTAKWTKVCAPCPDHYHYTDSWHTSDECL 60
Db 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKHCTAKWTKVCAPCPDHYHYTDSWHTSDECL 60
Qy 61 YCSPVCKELQVVKQECNRTHNRVCECKEGYLEIEFCLKHRSCTPPGPGVQAGTPERTV 120
Db 61 YCSPVCKELQVVKQECNRTHNRVCECKEGYLEIEFCLKHRSCTPPGPGVQAGTPERTV 120
Qy 121 CKRCPDFFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQK-----V 174
Db 121 CKRCPDFFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQK-----V 174
Qy 181 DKHTCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
Db 175 DKHTCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 234
Qy 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 360
Db 295 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 354
Qy 361 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPG 406
Db 355 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPG 400

RESULT 6
AAY72919
ID AAY72919 standard; protein; 400 AA.
XX
AC AAY72919;
XX
AC
XX
DT 13-JUN-2001 (first entry)
DE
DE Human OPG (22-194 aa)-Fc region (lacking 1-5 residues) fusion protein.
XX
XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
XX therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
XX hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
XX osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
XX periodontal.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..173
FT /note= "Derived from human osteoprotegerin fragment (22-
FT 194 residues)"
FT Region 174
FT /label= Linker
FT Region 175..400
FT /note= Human IgG1 Fc region lacking 1-5 residues
XX
XX WO200118203-A1.
XX
XX 15-MAR-2001.
XX
XX 18-AUG-2000; 2000WO-US022797.
XX
XX 03-SEP-1999; 99US-00389782.
XX
XX (AMGE-) AMGEN INC.
XX

```

```

XX Dunstan CR, Wooden SK, Mann MB;
XX WPI; 2001-244572/25.
XX
XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
XX by e.g. osteoporosis, Paget's disease and osteomyelitis.
XX
XX Claim 7; Fig 5; 119pp; English.
XX
XX The present sequence is a fusion protein comprising a sequence derived
XX from human osteoprotegerin (OPG; 22-194 residues) which is fused with
XX human immunoglobulin G1 (IgG1) Fc region lacking 1-5 residues by a
XX linker. OPG negatively regulates the formation of osteoclasts in vitro
XX and in vivo. It blocks the differentiation of osteoclasts from monocyte
XX or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion
XX protein is administered for the treatment of bone loss resulting from
XX osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia
XX associated with surgery or steroid administration, osteonecrosis, bone
XX loss due to rheumatoid arthritis, periodontal bone loss, osteolytic
XX metastasis and/or prosthetic loosening
XX
XX Sequence 400 AA;
SQ

Query Match          97.9%; Score 2227; DB 4; Length 400;
Best Local Similarity 98.5%; Pred. No. 4.7e-128;
Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKHCTAKWTKVCAPCPDHYHYTDSWHTSDECL 60
Db 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKHCTAKWTKVCAPCPDHYHYTDSWHTSDECL 60
Qy 61 YCSPVCKELQVVKQECNRTHNRVCECKEGYLEIEFCLKHRSCTPPGPGVQAGTPERTV 120
Db 61 YCSPVCKELQVVKQECNRTHNRVCECKEGYLEIEFCLKHRSCTPPGPGVQAGTPERTV 120
Qy 121 CKRCPDFFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVT 180
Db 121 CKRCPDFFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQK-----V 174
Qy 181 DKHTCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
Db 175 DKHTCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 234
Qy 241 GVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 300
Db 235 GVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 294
Qy 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 360
Db 295 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 354
Qy 361 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPG 406
Db 355 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPG 400

RESULT 7
AAB66993
ID AAB66993 standard; protein; 422 AA.
XX
AC AAB66993;
XX
XX 19-APR-2001 (first entry)
XX
XX OPG-Fc.
XX
XX Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
XX multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
XX systemic lupus erythematosus; graft-versus-host disease; septic shock;
XX acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
XX coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
XX endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
XX

```

ischaemia; Parkinson's disease.
 Unidentified.
 WO200103719-A2.
 18-JAN-2001.
 07-JUL-2000; 2000WO-US018667.
 09-JUL-1999; 99US-00350670.
 09-DEC-1999; 99US-00457647.
 (AMGE-) AMGEN INC.
 Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
 WPI; 2001-103031/11.
 N-PSDB; AAF57869.
 Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an osteoprotegerin protein in conjunction with e.g. inhibitors of interleukin and tumor necrosis factor alpha.
 Disclosure; Fig 29; 316pp; English.
 The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAF66974-AAF66976) in conjunction with other substances such as tumour necrosis factor-alpha (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF) 1-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock
 Sequence 422 AA;
 Query Match 97.9%; Score 2227; DB 4; Length 422;
 Best Local Similarity 98.5%; Pred. No. 5e-128;
 Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
 1 ETFPKYLHYDEETSHQLLDCPKPPTYLKQHCATKWKTVCAPCPDHYTDSWHTSDECL 60
 22 ETFPKYLHYDEETSHQLLDCPKPPTYLKQHCATKWKTVCAPCPDHYTDSWHTSDECL 81
 61 YCSPVCKELQYKQENRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPTERTV 120
 82 YCSPVCKELQYKQENRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPTERTV 141
 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSESSTOKCGIDVTV 180
 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSESSTOK-----V 195
 181 DKTHTCPCPAPELIGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
 196 DKTHTCPCPAPELIGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 255
 241 GVEVHNATKPREQVNSTYRVVSVLTVLHQDLNKGKEYCKVSKNALPAPIEKTISKAK 300
 256 GVEVHNATKPREQVNSTYRVVSVLTVLHQDLNKGKEYCKVSKNALPAPIEKTISKAK 315
 301 GQRPFPQVTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTPPPVLDLS 360
 316 GQRPFPQVTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTPPPVLDLS 375

QY 361 DGSFFLYSKLTVDKSRWQGNVFSVMEALHNNHYTKLSLSPG 406
 DB 376 DGSFFLYSKLTVDKSRWQGNVFSVMEALHNNHYTKLSLSPG 421
 RESULT 8
 ABG71831
 ID ABG71831 standard; protein; 425 AA.
 AC ABG71831;
 DT 14-APR-2003 (first entry)
 DE Human OPG protein for expression in mammalian cells.
 KW RANKL; human receptor activator of NFkappaB; osteoprotegerin; OPG;
 KW RANK ligand; osteoclastogenesis; osteoclast inhibitor; gene therapy;
 KW osteoporosis; bone disease; human.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200264782-A2.
 XX 22-AUG-2002.
 PF 08-FEB-2002; 2002WO-DK000090.
 PR 09-FEB-2001; 2001DK-00000214.
 PR 09-FEB-2001; 2001US-0267843P.
 PR 23-MAR-2001; 2001DK-00000498.
 PR 23-MAR-2001; 2001US-0278320P.
 PA (MAY-) MAXYGEN HOLDINGS LTD.
 XX Haaning JM, Halkier T;
 PI WPI; 2002-691592/74.
 DR N-PSDB; ABS56347.
 PT Novel human receptor activator of NFkappaB (hRANK) or human
 PT osteoprotegerin (hOPG) variant polypeptides which bind to RANK ligand
 PT (RANKL) with equivalent binding affinity as hRANK or hOPG, useful for
 PT treating osteoporosis.
 PS Example 4; Fig 12; 129pp; English.
 CC This invention relates to a novel polypeptide having an amino acid
 CC sequence that is different from and is at least about 70% identical to
 CC the amino acid sequence of human receptor activator of NFkappaB (hRANK)
 CC or human osteoprotegerin (hOPG), and which has a binding affinity to RANK
 CC ligand (RANKL) that is at least as high as the binding affinity of hRANK
 CC or hOPG to RANKL, as determined by functional competition assay. The
 CC protein of the invention may have osteopathic activity and may act as a
 CC RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclast activity
 CC inhibitor. The nucleotide sequence shown in the invention may be used in
 CC gene therapy. The protein of the invention or fusion proteins comprising
 CC this protein are useful as a pharmaceutical, and in the preparation of a
 CC medicament for treating or preventing osteoporosis, or other bone
 CC diseases or diseases associated with binding of RANKL to the RANK
 CC receptor. A host cell containing a vector expressing the protein is
 CC useful for producing a polypeptide having binding affinity to RANKL,
 CC where the polypeptide comprises at least one N- or O-glycosylation site
 CC and the host cell is a eukaryotic host cell capable of in vivo
 CC glycosylation, and/or the polypeptide is subjected to conjugation to a
 CC non-polypeptide moiety in vitro. The protein of the invention has
 CC increased functional in vivo half-life and/or serum half-life compared to
 CC hRANK or hOPG and has an improved binding affinity to RANKL compared to
 CC the binding affinity of hRANK or hOPG to RANKL, as determined by a
 CC functional competition assay. The present sequence represents a human OPG
 CC protein modified for expression in a mammalian system, this sequence has
 CC the human OPG protein fused to a Leu-Glu dipeptide and amino acid

```

CC residues 247-475 of human IGG1
XX Sequence 425 AA;
SQ

Query Match          97.9%; Score 2226; DB 5; Length 425;
Best Local Similarity 98.3%; Pred. No. 5.8e-128;
Matches 399; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKDPCPGTYLKQHTAKWTVCAPCPDHYTDSWHTSDECL 60
DB 22 ETTPPKYLHYDEETSHQLLCKDPCPGTYLKQHTAKWTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGPGVVQAGTPERNTV 120
DB 82 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGPGVVQAGTPERNTV 141
QY 121 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKCGIDVT 180
DB 142 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQK--LEKSS 199
QY 181 DKHTHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYD 240
DB 200 DKHTHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYD 259
QY 241 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
DB 260 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 319
QY 301 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360
DB 320 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 379
QY 361 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
DB 380 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 425

RESULT 9
AAB80899
ID AAB80899 standard; protein; 407 AA.
XX
AC AAB80899;
XX
DT 31-MAY-2001 (first entry)
XX
DE Human OPG (22-194)-Fc fusion protein.
XX
KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
KW osteoclast formation inhibition; bone resorption inhibition;
KW immunoglobulin.
XX
OS Homo sapiens.
XX
PN WO200117543-A2.
XX
PD 15-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-US022806.
XX
PR 03-SEP-1999; 99US-00389545.
XX
PA (AMGE-) AMGEN INC.
XX
PI Dunstan CR;
XX
XX WPI; 2001-265936/27.
XX
XX Preventing or treating lytic bone diseases, particularly associated with
PT cancer or metastasis, by administering an osteoprotegrin polypeptide.
XX
PS Disclosure; Fig 3; 87pp; English.
XX

```

```

CC The present invention relates to a method for the prevention or treatment
CC of lytic bone disease or multiple myeloma. Also the method can be used
CC for preventing metastasis of cancer to bone or osteosclerotic bone
CC metastasis. The method comprises administering an OPG (osteoprotegrin)
CC polypeptide or OPG fusion protein. The present sequence is one such OPG
CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone
CC resorption) by blocking differentiation from monocytes/macrophage
CC precursors. The OPG polypeptide can be used in a method of preventing or
CC treating lytic bone disease, for preventing metastasis of cancer to bone
CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic
CC bone metastasis. The OPG fusion polypeptides are used in the prevention
CC or treatment of loss of bone mass, which occurs in conditions including
CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
CC congenital forms of osteoporosis (osteogenesis imperfecta,
CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and bone
CC due to immobilisation of extremities; Paget's disease of bone (osteitis
CC deformans) in adults and juveniles; osteomyelitis, or an infectious
CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
CC hyperthyroidism and renal function disorders; osteopaenia following
CC surgery, induced by steroid administration, and associated with disorders
CC of the small and large intestine and with chronic hepatic and renal
CC diseases; osteonecrosis, or bone cell death, associated with traumatic
CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
CC cell anaemia, systemic lupus erythematosus and other conditions; bone
CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
CC are also used in the replacement of structurally sound bone with
CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
CC in adults and juveniles; hyperparathyroidism, in congenital bone
CC disorders such as fibrous dysplasia, and in osteosclerotic bone
CC metastases. The OPG fusion proteins can exhibit increased circulating
CC half-lives and slower clearance times, thereby providing a more sustained
CC activity. The OPG fusion protein comprises a fragment of the human OPG
CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and
CC CH3 regions; see AAB80897-8)
XX
SQ Sequence 407 AA;

```

```

Query Match          97.8%; Score 2224.5; DB 4; Length 407;
Best Local Similarity 98.0%; Pred. No. 6.8e-128;
Matches 399; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKDPCPGTYLKQHTAKWTVCAPCPDHYTDSWHTSDECL 60
DB 1 ETTPPKYLHYDEETSHQLLCKDPCPGTYLKQHTAKWTVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGPGVVQAGTPERNTV 120
DB 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGPGVVQAGTPERNTV 120
QY 121 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKCGID-VT 179
DB 121 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKAAEPKS 180
QY 180 VDKHTHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 239
DB 181 CDKTHHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 240
QY 240 DGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 299
DB 241 DGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
QY 300 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 359
DB 301 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360
QY 360 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 406

```


osteoporosis, such as primary osteoporosis, endocrine osteoporosis (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and congenital forms of osteoporosis (osteogenesis imperfecta, homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis due to immobilisation of extremities; Paget's disease of bone (osteitis deformans) in adults and juveniles; osteomyelitis, or an infectious lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung and kidney) and haematologic malignancies (multiple myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with hyperthyroidism and renal function disorders; osteopaenia following surgery, induced by steroid administration, and associated with disorders of the small and large intestine and with chronic hepatic and renal diseases; osteonecrosis, or bone cell death, associated with traumatic injury or nontraumatic necrosis associated with Gaucher's disease, sickle cell anaemia, systemic lupus erythematosus and other conditions; bone loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis; prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins are also used in the replacement of structurally sound bone with disorganised bone as seen in Paget's disease of bone (osteitis deformans) in adults and juveniles; hyperparathyroidism, in congenital bone disorders such as fibrous dysplasia, and in osteosclerotic bone metastases. The OPG fusion proteins can exhibit increased circulating half-lives and slower clearance times, thereby providing a more sustained activity. The OPG fusion protein comprises a fragment of the human OPG protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and CH3 regions; see AAB80897-8)

Sequence 404 AA;

Query Match 96.4%; Score 2191; DB 4; Length 404;
 Best Local Similarity 97.5%; Pred. No. 7.6e-126;
 Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKDPCPPGYLKQHCTAKWKTVCAPCDHYTDSWHTSDECL 60
 DB 1 ETTPPKYLHYDEETSHQLLCKDPCPPGYLKQHCTAKWKTVCAPCDHYTDSWHTSDECL 60

QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIFCLKHRSCTPPGFGVVOAGTPERNVT 120
 DB 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIFCLKHRSCTPPGFGVVOAGTPERNVT 120

QY 121 CKPCPDGFFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKSGIDVTV 180
 DB 121 CKPCPDGFFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKSG--GGG 178

QY 181 DKHTCTPCPAPPELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
 DB 179 GGGGTCTPCPAPPELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 238

QY 241 GVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 300
 DB 239 GVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 298

QY 301 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLD 360
 DB 299 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLD 358

QY 361 DGSFFLYSKLTVDKSRWQQGNVSCFVSWMHEALHHYTKQSLSPG 406
 DB 359 DGSFFLYSKLTVDKSRWQQGNVSCFVSWMHEALHHYTKQSLSPG 404

RESULT 12

AAV72921
 ID AAV72921 standard; protein; 404 AA.
 XX
 AC AAV72921;
 XX
 DT 13-JUN-2001 (first entry)
 XX
 DE Human OPG (22-194 residues)-FcG10 fusion protein.
 XX
 KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis; hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis; osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1; periodontal.

Homo sapiens.

Key Location/Qualifiers
 Region 1. .173
 /note= "Derived from human osteoprotegerin fragment (22-194 residues)"
 Region 174. .182
 /label= Ser-(Gly)8 linker
 Region 183. .404
 /note= Corresponds to 10-231 residues of human IgG1 Fc region

W0200118203-A1.

15-MAR-2001.

18-AUG-2000; 2000WO-US022797.

03-SEP-1999; 99US-00389782.

(AMGE-) AMGEN INC.

Dunstan CR, Wooden SK, Mann MB;

WPI; 2001-244572/25.

Osteoprotegerin-Fc protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis.

Claim 7; Fig 7; 119pp; English.

The present sequence is a fusion protein comprising a sequence derived from human osteoprotegerin (OPG; 22-194 residues) which is fused with human immunoglobulin G1 (IgG1) FcG10 region (lacks 1-9 residues and has a Ser-(Gly)8 linker). OPG negatively regulates the formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion protein is administered for the treatment of bone loss resulting from osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteonecrosis, bone loss due to rheumatoid arthritis, administration, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic loosening

Sequence 404 AA;

Query Match 96.4%; Score 2191; DB 4; Length 404;
 Best Local Similarity 97.5%; Pred. No. 7.6e-126;
 Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKDPCPPGYLKQHCTAKWKTVCAPCDHYTDSWHTSDECL 60
 DB 1 ETTPPKYLHYDEETSHQLLCKDPCPPGYLKQHCTAKWKTVCAPCDHYTDSWHTSDECL 60

QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIFCLKHRSCTPPGFGVVOAGTPERNVT 120
 DB 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIFCLKHRSCTPPGFGVVOAGTPERNVT 120

QY 121 CKPCPDGFFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKSGIDVTV 180
 DB 121 CKPCPDGFFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKSG--GGG 178

QY 181 DKHTCTPCPAPPELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
 DB 179 GGGGTCTPCPAPPELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 238

QY 241 GVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 300
 DB 239 GVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 298

QY 301 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDLS 360
 DB 299 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDLS 358
 QY 361 DGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPG 406
 DB 359 DGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPG 404

RESULT 13
 ABJ37103
 ID ABJ37103 standard; protein; 659 AA.
 XX AC ABJ37103;
 XX DT 08-MAY-2003 (first entry)
 XX DE Concatameric immunoadhesion human protein sequence SEQ ID NO 12.
 XX KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
 KW KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
 KW KW dimeric protein; inflammation; septicemia; cytotoxicity;
 KW KW rheumatoid arthritis; cachexia; inflammation; human.
 XX OS Homo sapiens.
 XX FN WO2003010202-A1.
 XX PD 06-FEB-2003.
 XX PF 26-JUL-2002; 2002WO-KR001427.
 XX PR 26-JUL-2001; 2001KR-00045028.
 XX PA (MEDE-) MEDEXGEN CO LTD.
 XX PI Chung Y, Han J, Lee H, Choi E, Kim J;
 XX DR WPI; 2003-229639/22.
 XX DR N-PSDB; ABT32046.
 XX PT New concatameric protein having two soluble domains, useful for
 PT diagnosing and treating disorders associated with the dimeric protein or
 PT its glycosylated form, such as inflammation, septicemia, rheumatoid
 PT arthritis and cachexia.
 XX PS Claim 27; Page 148-152; 21pp; English.
 XX CC The invention relates to a novel concatameric protein comprising two
 CC soluble domains, in which an N-terminus of a soluble domain of a
 CC biologically active protein is linked to a C-terminus of an identical
 CC soluble domain or a different soluble domain of a biologically active
 CC protein. The methods and compositions of the present invention are useful
 CC for the diagnosis and treatment of disorders associated with dimeric
 CC protein or its glycosylated form, such as inflammation, septicemia,
 CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
 CC related diseases. This sequence represents the human concatameric protein
 CC of the invention
 XX SQ Sequence 659 AA;

Query Match 66.9%; Score 1521.5; DB 6; Length 659;
 Best Local Similarity 65.6%; Pred. No. 1.1e-84;
 Matches 296; Conservative 16; Mismatches 80; Indels 59; Gaps 5;

QY 9 HYDEETSHQLCDKPPGFLYKQHCCTAKWKTVCAPDPHYTDSWHTSDECLYCSPVCKE 68
 DB 214 YDQ--TAQMCCSKSPGQHAHVFTKTSYTDVDCSDSTYTQLNNWPECLSCGRSS 271
 QY 69 LQYVQECNRTNHRVCECKEGRYLI-----EFLKHRSCTPPGVVQAGTPERTNYCK 122
 DB 272 DQVETQACTREQNRICTCPGMYCALSKQEGCRLCAPLRKCRPGFVARPGTETSDVVC 331

QY 123 RCPDGFSSNETSKAPCRKHTNCSYFGLLLLTOKGNATHDNIC----- 164
 DB 332 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLFQ 387
 QY 165 --SGNSESTQKCGIDVTV-----DKTHTCPPCPAPELL 195
 DB 388 PVSTRSQHTOPTPEPSTAPSTSLIPMGSPSPAEGSTGDAEPKSCDKTHTCPPAPELL 447
 QY 196 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTPREQ 255
 DB 448 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTPREQ 507
 QY 256 YNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 315
 DB 508 YNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 567
 QY 316 DELTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 375
 DB 568 DELTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 627
 QY 376 RWOQGNVSCSVMHEALHNHYTQKSLSLSPG 406
 DB 628 RWOQGNVSCSVMHEALHNHYTQKSLSLSPG 658

RESULT 14
 ADQ79910
 ID ADQ79910 standard; protein; 659 AA.
 XX AC ADQ79910;
 XX DT 09-SEP-2004 (first entry)
 XX DE Human tumour necrosis factor receptor 2, mgTNFR2-TNFR2/Ig construct.
 XX KW Human; tumour necrosis factor receptor; TNFR1; TNFR2; CTLA4; CD2; IgG;
 KW KW immunoglobulin; concatameric fused dimer protein; immunoadhesin;
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN KR2004009997-A.
 XX PD 31-JAN-2004.
 XX PF 26-JUL-2002; 2002KR-00045921.
 XX PR 26-JUL-2002; 2002KR-00045921.
 XX PA (MEDE-) MEDEXGEN INC.
 XX PI Choi EY, Han JU, Jung YH, Kim JM, Lee HJ;
 XX DR WPI; 2004-458871/43.
 XX DR N-PSDB; ADQ79909.
 XX PT Concatameric immunoadhesin.
 XX PS Claim 27; SEQ ID NO 12; 129pp; Korean.
 XX CC The invention relates to a concatameric fused dimer protein and
 CC glycosylation modification protein providing concatameric immunoadhesin
 CC with improved efficacy and stability. The concatameric protein is
 CC characteristically formed by binding C-terminal of one biologically
 CC active protein with N-terminal of same or different biologically active
 CC protein, e.g. tumour necrosis factor receptors (TNFR1 and TNFR2), CD2 and
 CC CTLA4. Two monomer proteins which are formed by fusing the extracellular
 CC region of a protein participating in the same immune reaction to an
 CC immunoglobulin Fc fragment, bound together at a hinge region by
 CC disulphide bond to give the concatameric fused dimer protein, wherein the
 CC immunoglobulin is IgG. The present sequence represents a monomeric or

```
CC dimeric IgG fusion protein (or a dimeric fusion protein containing
XX engineered N-glycosylation sites, designated "mg").
SQ Sequence 659 AA;

Query Match      66.9%; Score 1521.5; DB 8; Length 659;
Best Local Similarity 65.6%; Pred. No. 1.1e-84;
Matches 296; Conservative 18; Mismatches 80; Indels 59; Gaps 5;

QY 9 HYDEETSHQLLCKDKPPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDCLYCSPVCKE 68
DB 214 YVDQ--TAQMCCKSKSPGQHAQVFCIKTSDTDCSDCEDSTYTQLMWNVPECLSCGRCS 271
QY 69 LQVVKQECNTHRVCECKEGRYLEI-----EFLKHRSCPPGFGVVGAGTPERNVTCK 122
DB 272 DQVETOACTREONRICTRPGWYCALSKQEGCRLCAPLRKCRPGFGVAREGTETSDVCK 331
QY 123 RCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNIC----- 164
DB 332 PCAPGTFSTNTSTDICRPHQICNVVAI-----PGNASMDAVCTSTPTSRMAPGAVHLPQ 387
QY 165 --SGNSESTQKCGIDVTV----- 195
DB 388 PVSTRSOHTQTPPEPTAPSTFLLPMGPSPPAEGSTGDAEPKSCDKTHTCCPCPAPELL 447
QY 196 GGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 255
DB 448 GGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 507
QY 256 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYVTLPPSR 315
DB 508 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYVTLPPSR 567
QY 316 DELTKQVSLTCLVKGFPYSDIAVEVESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKS 375
DB 568 DELTKQVSLTCLVKGFPYSDIAVEVESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKS 627
QY 376 RWOQGNVFCSCVMHEALHNNHYTKQSLSPG 406
DB 628 RWOQGNVFCSCVMHEALHNNHYTKQSLSPG 658

RESULT 15
ADM32913
ID ADM32913 standard; protein; 489 AA.
XX AC ADM32913;
XX DT 17-JUN-2004 (first entry)
XX DE Amino acid sequence of Enbrel (etanercept).
XX KW synonymous codon; translation efficiency; Enbrel; etanercept.
XX OS Synthetic.
XX PN WO2004024915-A1.
XX PD 25-MAR-2004.
XX PF 15-SEP-2003; 2003WO-AU001200.
XX PR 13-SEP-2002; 2002US-0410410P.
XX PA (UYQU ) UNIV QUEENSLAND.
XX PI Frazer IH;
XX DR WPI; 2004-270043/25.
XX DR N-PSDB; ADM32912, ADM32914.
XX PT Constructing a synthetic polynucleotide, useful for producing a
    polypeptide at a higher level in a Chinese Hamster Ovary cell, comprises
```

```
PT selecting a first codon of the parent polynucleotide for replacement with
XX a synonymous codon.
XX Example 1; Fig 1; 82pp; English.
CC The specification describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible at a different
CC level in a Chinese Hamster Ovary (CHO) cell compared to when using a
CC parent polynucleotide encoding the same polypeptide. The method comprises
CC selecting a first codon of the parent polynucleotide for replacement with
CC a synonymous codon, where the synonymous codon is selected on the basis
CC that it exhibits a different translational efficiency in the CHO cell
CC than the first codon in a comparison of translational efficiencies of
CC codons in test CHO cells. The method is useful for constructing synthetic
CC polynucleotides which are translated more efficiently, compared to the
CC parent polynucleotide. The present sequence represents Enbrel
CC (etanercept), a synthetic polynucleotide encoding a fusion protein
CC consisting of two soluble TNF receptors joined by the Fc fragment of a
CC human IgG1 molecule. The Enbrel polynucleotide was codon-modified, to
CC demonstrate the method of the invention.
XX SQ Sequence 489 AA;
```

```
Query Match      66.7%; Score 1516; DB 8; Length 489;
Best Local Similarity 65.3%; Pred. No. 1.6e-84;
Matches 294; Conservative 18; Mismatches 80; Indels 58; Gaps 5;

QY 9 HYDEETSHQLLCKDKPPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDCLYCSPVCKE 68
DB 45 YVDQ--TAQMCCKSKSPGQHAQVFCIKTSDTDCSDCEDSTYTQLMWNVPECLSCGRCS 102
QY 69 LQVVKQECNTHRVCECKEGRYLEI-----EFLKHRSCPPGFGVVGAGTPERNVTCK 122
DB 103 DQVETOACTREONRICTRPGWYCALSKQEGCRLCAPLRKCRPGFGVAREGTETSDVCK 162
QY 123 RCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNIC----- 164
DB 163 PCAPGTFSTNTSTDICRPHQICNVVAI-----PGNASMDAVCTSTPTSRMAPGAVHLPQ 218
QY 165 --SGNSESTQKCGIDVTV----- 196
DB 219 PVSTRSOHTQTPPEPTAPSTFLLPMGPSPPAEGSTGDEPKSCDKTHTCCPCPAPELLG 278
QY 197 GGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 256
DB 279 GGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 338
QY 257 NSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYVTLPPSRD 316
DB 339 NSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYVTLPPSR 398
QY 317 ELTKQVSLTCLVKGFPYSDIAVEVESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 376
DB 399 EMTKQVSLTCLVKGFPYSDIAVEVESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 458
QY 377 WQOQGNVFCSCVMHEALHNNHYTKQSLSPG 406
DB 459 WQOQGNVFCSCVMHEALHNNHYTKQSLSPG 488
```

Search completed: March 8, 2005, 14:38:18
Job time : 87.1551 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:28:42 ; Search time 22.1968 Seconds
(without alignments)
1365.399 Million cell updates/sec

Title: US-09-389-782A-6
Perfect score: 2274
Sequence: 1 ETTPPKYLHYDETSHQLC.....VMHEALHNHYTKSLSPG 406

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1507.5	66.3	486	1	US-08-243-010-1
2	1501	66.0	518	1	US-08-385-229-4
3	1501	66.0	518	4	US-09-579-845-1
4	1501	66.0	518	4	US-09-579-845-3
5	1349	59.3	360	3	US-09-180-100-11
6	1349	59.3	376	3	US-09-180-100-22
7	1338.5	58.9	398	4	US-09-612-033B-14
8	1330	58.5	438	1	US-08-097-827-11
9	1330	58.5	438	1	US-08-494-574-11
10	1311.5	57.7	424	3	US-09-333-593A-8
11	1263.5	55.6	911	2	US-08-484-438-10
12	1260	55.4	704	4	US-09-590-656-2
13	1260	55.4	704	4	US-09-733-764-2
14	1257.5	55.3	664	3	US-08-957-063-16
15	1257.5	55.3	664	3	US-09-487-685-16
16	1257.5	55.3	664	3	US-08-802-805D-16
17	1257.5	55.3	664	4	US-09-388-316C-16
18	1254.5	55.2	664	3	US-09-957-063-18
19	1254.5	55.2	664	3	US-09-487-685-18
20	1254.5	55.2	664	3	US-08-802-805D-18
21	1254.5	55.2	664	4	US-09-388-316C-18
22	1250	55.0	592	4	US-09-313-942-8
23	1247	54.8	397	4	US-09-854-864-18
24	1246.5	54.8	680	3	US-08-227-496C-15
25	1241	54.6	347	1	US-07-940-861-43
26	1241	54.6	347	1	US-08-459-512-43
27	1241	54.6	347	2	US-08-459-657-43

Query Match 66.3%; Score 1507.5; DB 1; Length 486;
Best Local Similarity 64.5%; Pred. No. 9.1e-117;

28	1241	54.6	347	2	US-08-460-132-43	Sequence 43, Appl
29	1241	54.6	347	3	US-08-466-465-8	Sequence 8, Appl
30	1241	54.6	347	4	US-09-730-465-8	Sequence 8, Appl
31	1241	54.6	347	5	PCT-US92-02050-43	Sequence 43, Appl
32	1240.5	54.6	449	3	US-08-897-236-23	Sequence 23, Appl
33	1240.5	54.6	449	4	US-09-500-253B-23	Sequence 23, Appl
34	1239.5	54.5	783	4	US-09-854-864-9	Sequence 9, Appl
35	1239.5	54.5	784	4	US-09-313-942-30	Sequence 30, Appl
36	1238.5	54.5	455	4	US-09-773-877B-24	Sequence 24, Appl
37	1236.5	54.4	387	1	US-08-470-299-4	Sequence 4, Appl
38	1236.5	54.4	547	4	US-09-746-359A-54	Sequence 54, Appl
39	1236.5	54.4	571	4	US-09-746-359A-53	Sequence 53, Appl
40	1235	54.3	396	2	US-08-784-512-3	Sequence 3, Appl
41	1235	54.3	396	3	US-09-176-228-3	Sequence 3, Appl
42	1234.5	54.3	331	3	US-09-178-869-2	Sequence 2, Appl
43	1234.5	54.3	331	4	US-09-761-413-2	Sequence 2, Appl
44	1234.5	54.3	388	3	US-09-131-247-16	Sequence 16, Appl
45	1234.5	54.3	388	4	US-09-784-623-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-243-010-1
; Sequence 1, Application US/08243010
; Patent No. 5639597
; GENERAL INFORMATION:
; APPLICANT: Lauffer, Leander
; APPLICANT: Zettlmeissel, Gerd
; TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
; TITLE OF INVENTION: Production and Use Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,010
; FILING DATE: 13-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/798,564
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: DE P 40 37 837.3
; FILING DATE: 28-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 02481-1132-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 486 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-243-010-1

QY 69 LQVVKQECNTHNRVCEKGRYLEI-----BFCLKHRSCTPPGFGVVGQAGTPERNTVCK 122
Db 132 DQVETQACTREONRICTCRPGWTCALSKQBGCRCLCAPLRKCRPGFGVAREGTSTDVVCK 191
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC----- 164
Db 192 PCAPGTFSNTSTSDICRPHQICNVVAI-----PQNASMDAVCTSTSTPSRSMAPGAVHLPQ 247
QY 165 --SGNSESTQKCGIDVT----- 196
Db 248 PVSTRSQHTQTPTEPSTAPSTSFLLPMGPSPPAEGSTGDEPKSCDKTHTCCPCPAPELLG 307
QY 197 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREEQY 256
Db 308 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREEQY 367
QY 257 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRD 316
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRD 427
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 376
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 487
QY 377 WQOQNVFSCSVMEALHNNHYTKQSLSLSPG 406
Db 488 WQOQNVFSCSVMEALHNNHYTKQSLSLSPG 517

RESULT 4

US-09-579-845-3

; Sequence 3, Application US/09579845

; Patent No. 6537540

; GENERAL INFORMATION:

; APPLICANT: Burestein, Haim

; APPLICANT: Stepan, Anthony M.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING

; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED

; TITLE OF INVENTION: DISORDERS

; FILE REFERENCE: 22627200420

; CURRENT APPLICATION NUMBER: US/09/579,845

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 518

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-579-845-3

Query Match 66.0%; Score 1501; DB 4; Length 518;
Best Local Similarity 64.7%; Pred. No. 3.4e-116;
Matches 291; Conservative 19; Mismatches 82; Indels 58; Gaps 5;
QY 9 HYDEETSHQLLCKDCKPPGTYLKHQCTAKWTCVACPCPDHYHYTDSWHTSDCLYCSVPCKE 68
Db 74 YIQD--TAQWCCSKCSGQHAQVFCITKTSITVCDSCEDSTYTQIWNWVPECLSGSRCS 131
QY 69 LQVVKQECNTHNRVCEKGRYLEI-----BFCLKHRSCTPPGFGVVGQAGTPERNTVCK 122
Db 132 DQVETQACTREONRICTCRPGWTCALSKQBGCRCLCAPLRKCRPGFGVAREGTSTDVVCK 191
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC----- 164
Db 192 PCAPGTFSNTSTSDICRPHQICNVVAI-----PQNASMDAVCTSTSTPSRSMAPGAVHLPQ 247
QY 165 --SGNSESTQKCGIDVT----- 196
Db 248 PVSTRSQHTQTPTEPSTAPSTSFLLPMGPSPPAEGSTGDEPKSCDKTHTCCPCPAPELLG 307

QY 197 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREEQY 256
Db 308 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREEQY 367
QY 257 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRD 316
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRD 427
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 376
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 487
QY 377 WQOQNVFSCSVMEALHNNHYTKQSLSLSPG 406
Db 488 WQOQNVFSCSVMEALHNNHYTKQSLSLSPG 517

RESULT 5

US-09-180-100-11

; Sequence 11, Application US/09180100

; Patent No. 6306395

; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, No. 6306395io

; APPLICANT: NAKAMURA, Shigekazu

; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE

; FILE REFERENCE: 1110-207P

; CURRENT APPLICATION NUMBER: US/09/180,100

; CURRENT FILING DATE: 1998-11-02

; EARLIER APPLICATION NUMBER: PCT/JP97/01502

; EARLIER FILING DATE: 1997-05-01

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 11

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-180-100-11

Query Match 59.3%; Score 1349; DB 3; Length 360;
Best Local Similarity 56.3%; Pred. No. 8.5e-104;
Matches 270; Conservative 15; Mismatches 60; Indels 62; Gaps 9;
QY 8 LHYDEETSHQLLCKDCKPPGTYLKHQCTAKW-KTVACPCPD-HYHYTDSWHTSDCLYCSVP 65
Db 7 LHHDGQFCHK-----PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCR-L 61
QY 66 CKELQVVKQES--CNRTHNRVCEKGRYLEIEFCLKHRSCTPP-----GFGVVGQAGTPERNT 119
Db 62 CDEGHGLEVEINCTRTQNTKCRCKPNFCNSTVC-----EHCDCPTCKEHLIKECTILTSNT 118
QY 120 VCKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 179
Db 119 KCKE--EGSRSNPKS----- 132
QY 180 VDKTHCTPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 239
Db 133 CDKTHCTPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 192
QY 240 DGVEVHNATKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 299
Db 193 DGVEVHNATKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 252
QY 300 KGQPREPPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 359
Db 253 KGQPREPPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 312
QY 360 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPG 406
Db 313 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPG 359

RESULT 6

US-09-180-100-22

; Sequence 22, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-22

Query Match 59.3%; Score 1349; DB 3; Length 376;
Best Local Similarity 66.3%; Pred. No. 9e-104;
Matches 270; Conservative 15; Mismatches 60; Indels 62; Gaps 9;

QY 8 LHYDEETSHOLLCKPCPGTYLKQHC-TAKW-KTVCAPCPD-HYTTSDSWHTSDECLYCSPV 65
DB 23 LHHGQFCHK-----PCPPGERKARDCTVNGDEPCVQCEGKEYTDKAHFFSKRCR-L 77
QY 66 CKELQVYKQE--CNRTHNRVCECKEGRYLEIEFCLKHSRSCPP-----GFGVVQAGTPERNT 119
DB 78 CDEGHGLEVEINCTRTQNTKCRCKPNFCNSTVC---EHCDCPTCKEHIKECTLSNT 134
QY 120 VKRCPCDPGFSNITSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 179
DB 135 KCKE--EGSRNPKS----- 148
QY 180 VDKHTTCCPCPAPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYV 239
DB 149 CDKHTTCCPCPAPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYV 208
QY 240 DGVENVNATKPREQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAK 299
DB 209 DGVENVNATKPREQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAK 268
QY 300 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEVESNGQPNNTKTPPVLD 359
DB 269 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEVESNGQPNNTKTPPVLD 328
QY 360 SDGSFPLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPG 406
DB 329 SDGSFPLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPG 375

RESULT 7
US-09-612-033B-14
; Sequence 14, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmsat2, a No. 6627199el Member of the TNF-Receptor Superfamily
; TITLE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: Consisting of Mus musculus sequences and
; OTHER INFORMATION: Immunoglobulin sequences
US-09-612-033B-14

Query Match 58.9%; Score 1338.5; DB 4; Length 398;
Best Local Similarity 66.4%; Pred. No. 7.2e-103;
Matches 263; Conservative 24; Mismatches 58; Indels 51; Gaps 7;

QY 12 ETSQHLICDKCPCPGTYLKQHC-TAKW-KTVCAPCPDHYTSDSWHTSDECLYCSPVCKELQ 70
DB 52 EYWSKDVCCNCSAGTFVKAPCEIPIHTQOCCEKCHPGTFTKDNVLDACILCS-TCDDQ 110
QY 71 YVQECNRTHNRVCECKEGRYLEIEFCLKHSRSCPPGFGVQAGTPERNTVCKRCPDGFS 130
DB 111 EMVADCSATSDRKCQCRGLYY-----YDPKF-----DESCRPTCKCPQ---- 149
QY 131 NETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTVDKHTTCCPCP 190
DB 150 -----GIPVQECNSTANTVCSSVSN-----VD-THTCPCP 181
QY 191 APPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYVGVENVNATK 250
DB 192 APPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYVGVENVNATK 241
QY 251 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKQPREPQVY 310
DB 242 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKQPREPQVY 301
QY 311 LPPSRDELTKNOVSLTCLVKGFPSDIAVEVESNGQPNNTKTPPVLDSDGSFPLYSLK 370
DB 302 LPPSRDELTKNOVSLTCLVKGFPSDIAVEVESNGQPNNTKTPPVLDSDGSFPLYSLK 361
QY 371 TVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPG 406
DB 362 TVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPG 397

RESULT 8
US-097-827-11
; Sequence 11, Application US/08097827
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; Goodwin, Ray
; Fanglow, William
; Gayle, Richard
; TITLE OF INVENTION: Novel Cytokine which is a Ligand for
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-Jul-1993
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-097-827-11

Query Match      58.5%; Score 1330; DB 1; Length 438;
Best Local Similarity 62.6%; Pred. No. 4.1e-102;
Matches 263; Conservative 23; Mismatches 80; Indels 54; Gaps 6;

QY 20 CDKCPGTYLKQHCCTAKWKTVCAPCPDHYTDD--SMHTSDCLYCSVPCKELQVYVQECN 77
Db 39 CRECPQGHGMVNRCDHTRDTLCHPCETGYNVAVYDTCKQCTQCNH--RSGSELKQNC 96
QY 78 RTHNRVCECKEGRYLEIFCLKHSRCPGPGVQAGTPERTVCKRCPDGPFPSNETSSKA 137
Db 97 PTQDTVCRCR-----PGTPRQDSGYKLGVDVCPGPHFS--PGNNQ 137
QY 138 PCRKHTNCSVFGLLLTQKGNATHDNICSGNS-----ESTQKCGIDVTV----- 180
Db 138 ACKPWNTNCTLSGKQTRHPASDLSLDAVCEDRSLATLLMETQRTFRTTQSTTVMPRTS 197
QY 181 -----DKHTTCCPCAPPELLGSPSVFLPPPKPDTLMISRTPEVTCVVVDV 226
Db 198 ELPSTPTLVPRSCDKTHTCPPCPAPEAGAPSVFLPPPKPDTLMISRTPEVTCVVVDV 257
QY 227 SHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNK 286
Db 258 SHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNK 317
QY 287 ALPAPIETKTSKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 346
Db 318 ALPAPIETKTSKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 377
QY 347 PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 406
Db 378 PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 437

RESULT 9
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine which is a ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
```

```
;
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-494-574-11

Query Match      58.5%; Score 1330; DB 1; Length 438;
Best Local Similarity 62.6%; Pred. No. 4.1e-102;
Matches 263; Conservative 23; Mismatches 80; Indels 54; Gaps 6;

QY 20 CDKCPGTYLKQHCCTAKWKTVCAPCPDHYTDD--SMHTSDCLYCSVPCKELQVYVQECN 77
Db 39 CRECPQGHGMVNRCDHTRDTLCHPCETGYNVAVYDTCKQCTQCNH--RSGSELKQNC 96
QY 78 RTHNRVCECKEGRYLEIFCLKHSRCPGPGVQAGTPERTVCKRCPDGPFPSNETSSKA 137
Db 97 PTQDTVCRCR-----PGTPRQDSGYKLGVDVCPGPHFS--PGNNQ 137
QY 138 PCRKHTNCSVFGLLLTQKGNATHDNICSGNS-----ESTQKCGIDVTV----- 180
Db 138 ACKPWNTNCTLSGKQTRHPASDLSLDAVCEDRSLATLLMETQRTFRTTQSTTVMPRTS 197
QY 181 -----DKHTTCCPCAPPELLGSPSVFLPPPKPDTLMISRTPEVTCVVVDV 226
Db 198 ELPSTPTLVPRSCDKTHTCPPCPAPEAGAPSVFLPPPKPDTLMISRTPEVTCVVVDV 257
QY 227 SHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNK 286
Db 258 SHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNK 317
QY 287 ALPAPIETKTSKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 346
Db 318 ALPAPIETKTSKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 377
QY 347 PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 406
Db 378 PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 437

RESULT 10
US-09-333-593A-8
; Sequence 8, Application US/09333593A
; Patent No. 6332269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEWSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 424
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
```


US-09-333-593A-8

Query Match 57.7%; Score 1311.5; DB 3; Length 424;
Best Local Similarity 67.4%; Pred. No. 1.3e-100;
Matches 262; Conservative 16; Mismatches 60; Indels 51; Gaps 8;

QY 23 CPPTGTYLKQCTAKWTVACPC-DHYTDSMHTSDECLYCSVCKELQVVKQECNRTHN 81
DB 81 CPPTGTHISED-----GRDCISCKYQDYSTQWMDLLFLCLCTR-CDSEVELSPCTTTRN 134
QY 82 RVCECKEGRYLE---TEFCLKHS-CPPGFGVVQAGTPERTVCKPCDGFSSNETSSKA 137
DB 135 TVCQCEGTREDESPDMCKRKTGCGPRGMVKVGDCTPMSDIEC----- 178
QY 138 PCRKHTNCVFGLLLTQKNATHDNCISGNSESTQKCGIDVTVDKTHCTPPCPAPELLGG 197
DB 179 -VHKGSRSI-----EGRGTEPK-----SADKTHCTPPCPAPELLGG 214
QY 198 PSVFLPPPKDMLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 257
DB 215 PSVFLPPPKDMLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 274
QY 258 STYRVVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAGQPREQVYTLPSRDE 317
DB 275 STYRVVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAGQPREQVYTLPSRDE 334
QY 318 LTRKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 377
DB 335 LTRKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 394
QY 378 QQGNVFCSCVMHEALHNHYTQKSLSLSPG 406
DB 395 QQGNVFCSCVMHEALHNHYTQKSLSLSPG 423

RESULT 11

US-08-484-438-10
; Sequence 10, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory D.
; APPLICANT: Culouscou, Jean-Michel
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Siegall, Clay B.
; APPLICANT: Hellstr m, Ingegerd
; APPLICANT: Hellstr m, Karl E.
; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,438
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,442
; FILING DATE: 14-OCT-1994
; APPLICATION NUMBER: US 08/150,704
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/981,165

RESULT 12

US-09-590-656-2
; Sequence 2, Application US/09590656
; Patent No. 6413932
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Borges, Luis G.
; APPLICANT: Fanslow, III, William C.
; TITLE OF INVENTION: TEK ANTAGONISTS
; FILE REFERENCE: 2900-A
; CURRENT APPLICATION NUMBER: US/09/590,656
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/137,889
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2

FILING DATE: 24-NOV-1992

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,972

REFERENCE/DOCKET NUMBER: 5624-230

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 911 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-484-438-10

Query Match

Best Local Similarity 55.6%; Score 1263.5; DB 2; Length 911;

Matches 268; Conservative 23; Mismatches 46; Indels 115; Gaps 17;

QY 31 QHCTAKWTVACPCDPHYTDS--WHTS-DECLYC-----SPVCKELQVVKQECNRTHN 82

DB 494 ENCTAE-GMVC-----NHLCSGDCGCGPGDQCLSCRRFSRGRICIE----- 534

QY 83 VCECKEGRYLE---FCLKHS-CPPGFGVVQAGT-----PERNTVC-----K 122

DB 535 SCNLYDGBREFENGSIQVE---CDPQCEKMEGDLTCHGPGPDNCTKCSHPKDGPNQV 591

QY 123 RCPDGF-----FSNETSKAPCRKHTNCVFGLLTQ--KGNATHDNI---CSGNS 168

DB 592 KCPDQLQGANSTFKYADPDRECHPC--HPNC-----TQCCNGPTSHDCLYIYPTWTHS 642

QY 169 -----ESTQKCGIDVTVDKTHCTPPCPAP 192

DB 643 TLPQDPVKVKALEGPPRLVGPDPFGCAEPANTFLDPEPKSC-----DKHTCTPPCPAP 696

QY 193 ELLGGPSVFLPPPKDMLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 252

DB 697 ELLGGPSVFLPPPKDMLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 756

QY 253 EEQYNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAGQPREQVYTL 312

DB 757 EEQYNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAGQPREQVYTL 816

QY 313 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 372

DB 817 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 876

QY 373 DKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 406

DB 877 DKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 910

Query Match	55.4%	Score 1260	DB 4	Length 704
Best Local Similarity	58.0%	Pred. No. 4.9e-96		
Matches 276	Conservative	20	Mismatches 74	Indels 106
Query Match	55.3%	Score 1257.5	DB 3	Length 664
Best Local Similarity	58.0%	Pred. No. 4.9e-96		
Matches 276	Conservative	20	Mismatches 74	Indels 106
Query Match	55.4%	Score 1260	DB 4	Length 704
Best Local Similarity	58.0%	Pred. No. 4.9e-96		
Matches 276	Conservative	20	Mismatches 74	Indels 106
Query Match	55.3%	Score 1257.5	DB 3	Length 664
Best Local Similarity	58.0%	Pred. No. 4.9e-96		
Matches 276	Conservative	20	Mismatches 74	Indels 106

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:44:50 ; Search time 61.3439 Seconds
(without alignments)
2177.757 Million cell updates/sec

Title: US-09-389-782A-6

Perfect score: 2274

Sequence: 1 ETTPPKYLHYDEETSHQLLC.....VMHEALHNYTKSLSPG 406

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 32904822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB-seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2274	100.0	406	10	US-09-389-782-6
2	2256.5	99.2	413	10	US-09-389-782-4
3	2227	97.9	400	10	US-09-389-782-5
4	2226	97.9	425	16	US-10-467-243-20
5	2224.5	97.8	407	10	US-09-389-782-3
6	2191	96.4	404	10	US-09-389-782-7
7	1521.5	66.9	659	14	US-10-363-427-12
8	1516	66.7	467	17	US-10-901-735-4
9	1513.5	66.6	490	14	US-10-363-427-4
10	1513.5	66.6	720	14	US-10-363-427-8
11	1501	66.0	518	14	US-10-313-852-1
12	1501	66.0	518	14	US-10-313-852-3
13	1501	66.0	518	14	US-10-314-033-1

14	1501	66.0	518	14	US-10-314-033-3	Sequence 3, Appli
15	1501	66.0	518	15	US-10-423-507-1	Sequence 1, Appli
16	1470.5	64.7	444	16	US-10-467-243-24	Sequence 24, Appl
17	1458.5	64.1	443	14	US-10-151-071-5	Sequence 5, Appli
18	1458.5	64.1	443	14	US-10-166-232A-5	Sequence 5, Appli
19	1389.5	61.1	608	14	US-10-363-427-10	Sequence 10, Appl
20	1381.5	60.8	444	14	US-10-363-427-2	Sequence 2, Appli
21	1381.5	60.8	628	14	US-10-363-427-6	Sequence 6, Appli
22	1349	59.3	360	9	US-09-949-713-11	Sequence 11, Appl
23	1349	59.3	376	9	US-09-949-713-22	Sequence 22, Appl
24	1349	59.3	376	14	US-10-084-139-10	Sequence 10, Appl
25	1348.5	59.3	396	14	US-10-193-616-14	Sequence 14, Appl
26	1338.5	58.9	398	15	US-10-622-407-14	Sequence 14, Appl
27	1287.5	56.6	380	9	US-09-948-018-39	Sequence 39, Appl
28	1277	56.2	404	9	US-09-948-018-16	Sequence 16, Appl
29	1275	56.1	446	9	US-09-792-200B-10	Sequence 10, Appl
30	1268	55.8	334	15	US-10-258-368-8	Sequence 8, Appli
31	1268	55.8	366	15	US-10-258-368-6	Sequence 6, Appli
32	1261	55.5	542	9	US-09-792-200B-16	Sequence 16, Appl
33	1260	55.4	704	9	US-09-733-764-2	Sequence 2, Appli
34	1260	55.4	704	14	US-10-357-653-2	Sequence 20, Appl
35	1258	55.3	360	15	US-10-390-566-20	Sequence 20, Appl
36	1258	55.3	360	15	US-10-390-566-27	Sequence 27, Appl
37	1258	55.3	367	15	US-10-390-566-19	Sequence 19, Appl
38	1258	55.3	367	15	US-10-390-566-26	Sequence 26, Appl
39	1258	55.3	404	15	US-10-258-368-15	Sequence 15, Appl
40	1257.5	55.3	664	9	US-09-388-316-16	Sequence 16, Appl
41	1257.5	55.3	664	14	US-10-357-822-16	Sequence 7, Appli
42	1257	55.3	360	15	US-10-390-566-7	Sequence 7, Appli
43	1257	55.3	360	15	US-10-390-566-14	Sequence 14, Appl
44	1257	55.3	367	15	US-10-390-566-6	Sequence 6, Appli
45	1257	55.3	367	15	US-10-390-566-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-389-782-6
; Sequence 6, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Human
; US-09-389-782-6

Query Match	100.0%	Score	2274;	DB	10;	Length	406;
Best Local Similarity	100.0%	Pred. No.	1.4e-139;				
Matches	406;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
Qy	1	ETTPPKYLHYDEETSHQLLCDCPPGTYLKQHTAKWTVCA	CPDHYTDSWHTSDECL	60			
Db	1	ETTPPKYLHYDEETSHQLLCDCPPGTYLKQHTAKWTVCA	CPDHYTDSWHTSDECL	60			
Qy	61	YCSFVCKEYQVKEQNRTHNRVCEKGEKYLEIECLKXHS	CPGPGVVOAGTPERTV	120			
Db	61	YCSFVCKEYQVKEQNRTHNRVCEKGEKYLEIECLKXHS	CPGPGVVOAGTPERTV	120			
Qy	121	CKRCPDGFSTNETSSKAPCKKHTNCVFGLLLTQKGNATH	DNICSGNSESTQKCGIDTV	180			
Db	121	CKRCPDGFSTNETSSKAPCKKHTNCVFGLLLTQKGNATH	DNICSGNSESTQKCGIDTV	180			

QY 181 DKHTCCPCAPPELLGGPSVFLPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
Db 181 DKHTCCPCAPPELLGGPSVFLPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
QY 241 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
Db 241 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
Db 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
QY 361 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTKQSLSPG 406
Db 361 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTKQSLSPG 406

RESULT 2
US-09-389-782-4
; Sequence 4, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-4

Query Match 99.2%; Score 2256.5; DB 10; Length 413;
Best Local Similarity 98.1%; Pred. No. 1.9e-138;
Matches 405; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
QY 1 ETPFPKYLHYDEETSHQLLCKDCPPGTLYLKQHTAKWKTVCAPCDPDHYTDSWHTSDECL 60
Db 1 ETPFPKYLHYDEETSHQLLCKDCPPGTLYLKQHTAKWKTVCAPCDPDHYTDSWHTSDECL 60
QY 61 YCSPVKELQYVKQECNTRNHRVCECKEGRYLEIEFCLKHSRCPGPGFVGVQAGTPTERTV 120
Db 61 YCSPVKELQYVKQECNTRNHRVCECKEGRYLEIEFCLKHSRCPGPGFVGVQAGTPTERTV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVT 180
Db 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVT 180
QY 181 -----DKHTCCPCAPPELLGGPSVFLPPKPKOTLMISRTPEVTCVVVDVSHEDPEV 233
Db 181 AAEPSKCDKHTCCPCAPPELLGGPSVFLPPKPKOTLMISRTPEVTCVVVDVSHEDPEV 240
QY 234 KFNWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 293
Db 241 KFNWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 300
QY 294 KTIISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 353
Db 301 KTIISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 360
QY 354 TTPVLDSGSPFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTKQSLSPG 406
Db 361 TTPVLDSGSPFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTKQSLSPG 413

RESULT 3
US-09-389-782-5
; Sequence 5, Application US/09389782

; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-5

Query Match 97.9%; Score 2227; DB 10; Length 400;
Best Local Similarity 98.5%; Pred. No. 1.5e-136;
Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
QY 1 ETPFPKYLHYDEETSHQLLCKDCPPGTLYLKQHTAKWKTVCAPCDPDHYTDSWHTSDECL 60
Db 1 ETPFPKYLHYDEETSHQLLCKDCPPGTLYLKQHTAKWKTVCAPCDPDHYTDSWHTSDECL 60
QY 61 YCSPVKELQYVKQECNTRNHRVCECKEGRYLEIEFCLKHSRCPGPGFVGVQAGTPTERTV 120
Db 61 YCSPVKELQYVKQECNTRNHRVCECKEGRYLEIEFCLKHSRCPGPGFVGVQAGTPTERTV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVT 180
Db 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVT 180
QY 181 DKHTCCPCAPPELLGGPSVFLPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
Db 175 DKHTCCPCAPPELLGGPSVFLPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 234
QY 241 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
Db 235 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 294
QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
Db 295 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 354
QY 361 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTKQSLSPG 406
Db 355 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTKQSLSPG 400

RESULT 4
US-10-467-243-20
; Sequence 20, Application US/10467243
; Publication No. US20040132971A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Holdings Ltd.
; APPLICANT: Haaning, Jesper Mortensen
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES
; FILE REFERENCE: 0226w0310
; CURRENT APPLICATION NUMBER: US/10/467,243
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: DK PA 2001 00214
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/267,843
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00498
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/278,320
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20

```
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPG-Fc polypeptide encoded by SEQ ID NO:19
US-10-467-243-20

Query Match      97.9%; Score 2226; DB 16; Length 425;
Best Local Similarity 98.3%; Pred. No. 1.9e-136;
Matches 399; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 22  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81

QY 61  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHRSCPPGFGVVQAGTPERNIV 120
Db 82  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHRSCPPGFGVVQAGTPERNIV 141

QY 121  CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTV 180
Db 142  CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQK--LEKSS 199

QY 181  DKTHTCPPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYD 240
Db 200  DKTHTCPPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYD 259

QY 241  GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
Db 260  GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 319

QY 301  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360
Db 320  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 379

QY 361  DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPG 406
Db 380  DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPG 425

RESULT 5
US-09-389-782-3
; Sequence 3, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-3

Query Match      97.8%; Score 2224.5; DB 10; Length 407;
Best Local Similarity 98.0%; Pred. No. 2.3e-136;
Matches 399; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 1  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60

QY 61  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHRSCPPGFGVVQAGTPERNIV 120
Db 61  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHRSCPPGFGVVQAGTPERNIV 120

QY 121  CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGID-VT 179

; LENGTH: 425
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPG-Fc polypeptide encoded by SEQ ID NO:19
US-10-467-243-20

Query Match      97.9%; Score 2226; DB 16; Length 425;
Best Local Similarity 98.3%; Pred. No. 1.9e-136;
Matches 399; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 22  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81

QY 61  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHRSCPPGFGVVQAGTPERNIV 120
Db 82  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHRSCPPGFGVVQAGTPERNIV 141

QY 121  CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTV 180
Db 142  CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQK--LEKSS 199

QY 181  DKTHTCPPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYD 240
Db 200  DKTHTCPPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYD 259

QY 241  GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
Db 260  GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 319

QY 301  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360
Db 320  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 379

QY 361  DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPG 406
Db 380  DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPG 425

RESULT 6
US-09-389-782-7
; Sequence 7, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-7

Query Match      96.4%; Score 2191; DB 10; Length 404;
Best Local Similarity 97.5%; Pred. No. 3.4e-134;
Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 1  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 1  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60

QY 61  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHRSCPPGFGVVQAGTPERNIV 120
Db 61  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHRSCPPGFGVVQAGTPERNIV 120

QY 121  CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTV 180
Db 121  CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKSG--GGG 178

QY 181  DKTHTCPPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYD 240
Db 179  GGGGTCCPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYD 238

QY 241  GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
Db 239  GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 298

QY 301  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360
Db 299  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 358

QY 361  DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPG 406
Db 359  DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPG 404
```

RESULT 7

US-10-363-427-12
; Sequence 12, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: MedexGen Inc.

; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin

; TITLE OF INVENTION: Concatametric Immunoadhesion

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/363,427

; CURRENT FILING DATE: 2003-02-28

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: Kopatentin 1.71

; SEQ ID NO 12

; LENGTH: 659

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-363-427-12

Query Match 66.9%; Score 1521.5; DB 14; Length 659;

Best Local Similarity 65.6%; Pred. No. 1.5e-90;

Matches 296; Conservative 16; Mismatches 80; Indels 59; Gaps 5;

QY 9 HYDEETSHOLLCDKCPGGTYLKQHTAKWKTVCAPCPDHYHYTDSWHTDECLYCSPVCKE 68

DB 214 YDQ--TAQMCCKSGPGQHAQVCTKTSDTVCDSCDSTYQLMNNVPECLSCGSRCS 271

QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGGVGVQAGTPERNTVCK 122

DB 272 DQVETQACTREQNRICTRPGMYCALSKQEGCRLCAPLRCRPGFVGARPGTETSDVCK 331

QY 123 RCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHNIC----- 164

DB 332 PCAPGTFTNTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTPTSRMAPGAVHLPQ 387

QY 165 --SGNSESTQKCGIDTVV-----DKHTTCCPPCAPELL 195

DB 388 PVSTRSQHTOPTPEPTASTSTFLLPMGPPSPAGSTGDAEPKSCDKTHTCCPPCAPELL 447

QY 196 GGPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQ 255

DB 448 GGPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQ 507

QY 256 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 315

DB 508 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 567

QY 316 DELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDK 375

DB 568 DELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDK 627

QY 376 RWQGNVFCVSMHEALHNHYTQKSLSLSPG 406

DB 628 RWQGNVFCVSMHEALHNHYTQKSLSLSPG 658

RESULT 8

US-10-901-735-4

; Sequence 4, Application US/10901735

; Publication No. US20050032183A1

; GENERAL INFORMATION:

; APPLICANT: AMGEN, Inc.

; APPLICANT: OSSUND, Timothy D.

; APPLICANT: CLOSTON, Christi

; APPLICANT: CRAMPTON, Shon

; APPLICANT: BASS, Randal

; TITLE OF INVENTION: CRYSTALLINE POLYPEPTIDES

; FILE REFERENCE: A-859

; CURRENT APPLICATION NUMBER: US/10/901,735

; CURRENT FILING DATE: 2004-07-29

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 4

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Fusion polypeptide

US-10-901-735-4

Query Match 66.7%; Score 1516; DB 17; Length 467;

Best Local Similarity 65.3%; Pred. No. 2.3e-90;

Matches 294; Conservative 18; Mismatches 80; Indels 58; Gaps 5;

QY 9 HYDEETSHOLLCDKCPGGTYLKQHTAKWKTVCAPCPDHYHYTDSWHTDECLYCSPVCKE 68

DB 23 YDQ--TAQMCCKSGPGQHAQVCTKTSDTVCDSCDSTYQLMNNVPECLSCGSRCS 80

QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGGVGVQAGTPERNTVCK 122

DB 81 DQVETQACTREQNRICTRPGMYCALSKQEGCRLCAPLRCRPGFVGARPGTETSDVCK 140

QY 123 RCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHNIC----- 164

DB 141 PCAPGTFTNTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTPTSRMAPGAVHLPQ 196

QY 165 --SGNSESTQKCGIDTVV-----DKHTTCCPPCAPELL 196

DB 197 PVSTRSQHTOPTPEPTASTSTFLLPMGPPSPAGSTGDEPKSCDKTHTCCPPCAPELL 256

QY 197 GGPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQ 256

DB 257 GGPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQ 316

QY 257 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 316

DB 317 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 376

QY 317 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDK 376

DB 377 EMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDK 436

QY 377 WQGNVFCVSMHEALHNHYTQKSLSLSPG 406

DB 437 WQGNVFCVSMHEALHNHYTQKSLSLSPG 466

RESULT 9

US-10-363-427-4

; Sequence 4, Application US/10363427

; Publication No. US20030195338A1

; GENERAL INFORMATION:

; APPLICANT: MedexGen Inc.

; APPLICANT: CHUNG, Yong Hoon

; APPLICANT: HAN, Ji Woong

; APPLICANT: LEE, Hye Ja

; APPLICANT: CHOI, Eun Yong

; APPLICANT: KIM, Jin Mi

; APPLICANT: YIM, Soo Bin

; TITLE OF INVENTION: Concatametric Immunoadhesion

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/363,427

; CURRENT FILING DATE: 2003-02-28

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: Kopatentin 1.71

; SEQ ID NO 4

; LENGTH: 490

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-363-427-4

```
Query Match      66.6%; Score 1513.5; DB 14; Length 490;
Best Local Similarity 65.4%; Pred. No. 3.5e-90;
Matches 295; Conservative 16; Mismatches 81; Indels 59; Gaps 5;

QY 9 HYDETSQHLCDKCPGTYLKHQCTAKWTVCAPCPDHYITDSWHTSDCLYCSPVCKE 68
DB 45 YYDQ--TAQCCSKCSPGQAHKVFCTKTSDTVCDSCEDSTYTQLWNWPECLSGRCSS 102

QY 69 LOYVQECNRTNVRCECKEGRYLEI-----EFCLKHRSCTPGFGVQAGTPERNTVCK 122
DB 103 DQVETOACTREQNRICTCRPGWYCALSKQEGCLCAPLRCRPGFGVARGTETSDVCK 162

QY 123 RCPDGFSSNETSKAPCRKHTNCSVFGLLLTOKGNATHDNIC----- 164
DB 163 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTPTSRMAPGAVHLPQ 218

QY 165 --SGNSESTQKCGIDVTV----- 406
DB 219 PVSTRSQHTOPTPEPSTAPSTSFLLPMGPPSPAGSTGDAEPKSCDKTHTCPCPAPELL 278

QY 196 GGPVSFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREEQ 255
DB 279 GGPVSFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREEQ 338

QY 256 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 315
DB 339 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 398

QY 316 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKTVDKS 375
DB 399 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKTVDKS 458

QY 376 RWOQGNVFCSCVMHEALHNYTKQSLSLSPG 406
DB 459 RWOQGNVFCSCVMHEALHNYTKQSLSLSPG 489

RESULT 10
US-10-363-427-8
; Sequence 8, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: MedexGen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatametric Immunoadhesion
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 8
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-427-8

Query Match      66.6%; Score 1513.5; DB 14; Length 720;
Best Local Similarity 65.4%; Pred. No. 5.3e-90;
Matches 295; Conservative 16; Mismatches 81; Indels 59; Gaps 5;

QY 9 HYDETSQHLCDKCPGTYLKHQCTAKWTVCAPCPDHYITDSWHTSDCLYCSPVCKE 68
DB 275 YYDQ--TAQCCSKCSPGQAHKVFCTKTSDTVCDSCEDSTYTQLWNWPECLSGRCSS 332

QY 69 LOYVQECNRTNVRCECKEGRYLEI-----EFCLKHRSCTPGFGVQAGTPERNTVCK 122
DB 333 DQVETOACTREQNRICTCRPGWYCALSKQEGCLCAPLRCRPGFGVARGTETSDVCK 392
```

```
QY 123 RCPDGFSSNETSKAPCRKHTNCSVFGLLLTOKGNATHDNIC----- 164
DB 393 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTPTSRMAPGAVHLPQ 448

QY 165 --SGNSESTQKCGIDVTV----- 406
DB 449 PVSTRSQHTOPTPEPSTAPSTSFLLPMGPPSPAGSTGDAEPKSCDKTHTCPCPAPELL 508

QY 196 GGPVSFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREEQ 255
DB 509 GGPVSFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREEQ 568

QY 256 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 315
DB 569 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 628

QY 316 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKTVDKS 375
DB 629 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKTVDKS 688

QY 376 RWOQGNVFCSCVMHEALHNYTKQSLSLSPG 406
DB 689 RWOQGNVFCSCVMHEALHNYTKQSLSLSPG 719

RESULT 11
US-10-313-852-1
; Sequence 1, Application US/10313852
; Publication No. US20030103942A1
; GENERAL INFORMATION:
; APPLICANT: Bursstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/313,852
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-313-852-1

Query Match      66.0%; Score 1501; DB 14; Length 518;
Best Local Similarity 64.7%; Pred. No. 2.4e-89;
Matches 291; Conservative 19; Mismatches 82; Indels 58; Gaps 5;

QY 9 HYDETSQHLCDKCPGTYLKHQCTAKWTVCAPCPDHYITDSWHTSDCLYCSPVCKE 68
DB 74 YYDQ--TAQCCSKCSPGQAHKVFCTKTSDTVCDSCEDSTYTQLWNWPECLSGRCSS 131

QY 69 LOYVQECNRTNVRCECKEGRYLEI-----EFCLKHRSCTPGFGVQAGTPERNTVCK 122
DB 132 DQVETOACTREQNRICTCRPGWYCALSKQEGCLCAPLRCRPGFGVARGTETSDVCK 191

QY 123 RCPDGFSSNETSKAPCRKHTNCSVFGLLLTOKGNATHDNIC----- 164
DB 192 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTPTSRMAPGAVHLPQ 247

QY 165 --SGNSESTQKCGIDVTV----- 406
DB 248 PVSTRSQHTOPTPEPSTAPSTSFLLPMGPPSPAGSTGDAEPKSCDKTHTCPCPAPELL 307

QY 197 GGPVSFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREEQ 256
DB 308 GGPVSFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREEQ 367
```


QY 257 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 316
Db 368 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPMOKTISKAKGQPREPQVYTLPPSRD 427
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 376
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 487
QY 377 WOQGNVFCSCVMHEALHNHYTQKSLSLSPG 406
Db 488 WOQGNVFCSCVMHEALHNHYTQKSLSLSPG 517

RESULT 12
US-10-313-852-3
; Sequence 3, Application US/10313852
; Publication No. US20030103942A1
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/313,852
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-313-852-3

Query Match 66.0%; Score 1501; DB 14; Length 518;
Best Local Similarity 64.7%; Pred. No. 2.4e-89;
Matches 291; Conservative 19; Mismatches 82; Indels 58; Gaps 5;

QY 9 HYDETSQLLCDKCPGTYLKHQCTAKWKTVCAPCPDHYHYTDSWHTSDECLYCSPVCKE 68
Db 74 YDQ--TAQMCCKSCSPGQAHKVFCTKTSVDCSDSTYTQLMNWPVCLSCGSRCS 131
QY 69 LQYVKQECNTHNRVCECKEGRYLEI-----EFLKHRSCPPGFGVQVQAGTPERNTVCK 122
Db 132 DQVETOACTREQNRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVQVQAGTPERNTVCK 191
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNC-----164
Db 192 PCAGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247
QY 165 --SGNSESTQKCGIDVTV-----DKHTTCCPCPAPPELLG 196
Db 248 PVSTRSQHTQTPERPSTAPSTSFLLPMGSPPAEGSTGDEPKSCDKTHTCCPCPAPPELLG 307
QY 197 GPSVFLPPPKDQTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 256
Db 308 GPSVFLPPPKDQTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 367
QY 257 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 316
Db 368 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPMOKTISKAKGQPREPQVYTLPPSRD 427
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 376
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 487
QY 377 WOQGNVFCSCVMHEALHNHYTQKSLSLSPG 406
Db 488 WOQGNVFCSCVMHEALHNHYTQKSLSLSPG 517

Db 488 WOQGNVFCSCVMHEALHNHYTQKSLSLSPG 517

RESULT 13
US-10-314-033-1
; Sequence 1, Application US/10314033
; Publication No. US20030113295A1
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/314,033
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-033-1

Query Match 66.0%; Score 1501; DB 14; Length 518;
Best Local Similarity 64.7%; Pred. No. 2.4e-89;
Matches 291; Conservative 19; Mismatches 82; Indels 58; Gaps 5;

QY 9 HYDETSQLLCDKCPGTYLKHQCTAKWKTVCAPCPDHYHYTDSWHTSDECLYCSPVCKE 68
Db 74 YDQ--TAQMCCKSCSPGQAHKVFCTKTSVDCSDSTYTQLMNWPVCLSCGSRCS 131
QY 69 LQYVKQECNTHNRVCECKEGRYLEI-----EFLKHRSCPPGFGVQVQAGTPERNTVCK 122
Db 132 DQVETOACTREQNRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVQVQAGTPERNTVCK 191
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNC-----164
Db 192 PCAGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247
QY 165 --SGNSESTQKCGIDVTV-----DKHTTCCPCPAPPELLG 196
Db 248 PVSTRSQHTQTPERPSTAPSTSFLLPMGSPPAEGSTGDEPKSCDKTHTCCPCPAPPELLG 307
QY 197 GPSVFLPPPKDQTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 256
Db 308 GPSVFLPPPKDQTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 367
QY 257 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 316
Db 368 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPMOKTISKAKGQPREPQVYTLPPSRD 427
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 376
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 487
QY 377 WOQGNVFCSCVMHEALHNHYTQKSLSLSPG 406
Db 488 WOQGNVFCSCVMHEALHNHYTQKSLSLSPG 517

RESULT 14
US-10-314-033-3
; Sequence 3, Application US/10314033
; Publication No. US20030113295A1
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING

```
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; FILE REFERENCE: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/314,033
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-314-033-3

Query Match      66.0%; Score 1501; DB 14; Length 518;
Best Local Similarity 64.7%; Pred. No. 2.4e-89;
Matches 291; Conservative 19; Mismatches 82; Indels 58; Gaps 5;

QY 9 HYDEETSHQLCDKCPGGTYLKQHTAKWKTCVACPCPDHYHDTSDWHTSDECLYCSPVCKE 68
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 74 YYDQ--TAQMCCKSGSPGQHAQVCTKTSDTVCDSCESTYTQLMNNVPECLSCGSRCS 131
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFLKHRSCPPGPGVVOAGTPERTNVCK 122
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 132 DQVETOACTREQNRICTRCPGMYCALSKQEGCRLCAPLRKCRPGFGVARGPTETSDVVC 191
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 123 RCPDGFPSNETSKAPCRKHTNCVSFGLLLTKQGNATHDNIC----- 164
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 192 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 165 --SGNSESTQKCGIDVTV----- 248
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 248 PVSTRSQHTQPTPEPSTAPSTSFLLPMGPPSPAEAGSTGDEPKSCDKTHTCPCPAPPELLG 307
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 197 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQY 256
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 308 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQY 367
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 257 NSTYRVSVSLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 316
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 368 NSTYRVSVSLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 427
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 376
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 428 ELTKNQVSLTCLVKGFYPRHIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 487
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 377 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 406
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 488 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 517
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:

RESULT 15
US-10-423-507-1
; Sequence 1, Application US/10423507
; Publication No. US20030219735A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Barrie, J.
; TITLE OF INVENTION: METABOLICALLY ACTIVATED RECOMBINANT
; FILE REFERENCE: 226272004302
; CURRENT APPLICATION NUMBER: US/10/423,507
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 09/634,126
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 60/160,080
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-423-507-1

Query Match      66.0%; Score 1501; DB 15; Length 518;
Best Local Similarity 64.7%; Pred. No. 2.4e-89;
Matches 291; Conservative 19; Mismatches 82; Indels 58; Gaps 5;

QY 9 HYDEETSHQLCDKCPGGTYLKQHTAKWKTCVACPCPDHYHDTSDWHTSDECLYCSPVCKE 68
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 74 YYDQ--TAQMCCKSGSPGQHAQVCTKTSDTVCDSCESTYTQLMNNVPECLSCGSRCS 131
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFLKHRSCPPGPGVVOAGTPERTNVCK 122
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 132 DQVETOACTREQNRICTRCPGMYCALSKQEGCRLCAPLRKCRPGFGVARGPTETSDVVC 191
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 123 RCPDGFPSNETSKAPCRKHTNCVSFGLLLTKQGNATHDNIC----- 164
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 192 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 165 --SGNSESTQKCGIDVTV----- 248
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 248 PVSTRSQHTQPTPEPSTAPSTSFLLPMGPPSPAEAGSTGDEPKSCDKTHTCPCPAPPELLG 307
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 197 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQY 256
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 308 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQY 367
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 257 NSTYRVSVSLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 316
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 368 NSTYRVSVSLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 427
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 376
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 428 ELTKNQVSLTCLVKGFYPRHIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 487
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 377 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 406
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 488 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 517
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:

Search completed: March 8, 2005, 15:16:08
Job time : 66.3439 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:20:42 ; Search time 16.5467 Seconds
(without alignments)
2360.831 Million cell updates/sec

Title: US-09-389-782A-6
Perfect score: 2274
Sequence: 1 ETPPPKYLHYDETSQLLC.....VMHEALHNHYTKSLSLSPG 406
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1231	54.1	330	1 GHU	Ig gamma-1 chain C
2	1228	54.0	255	4 S31866	Ig gamma-1 chain C
3	1222.5	53.8	374	2 S69339	Ig heavy chain V x
4	1190	51.9	234	2 PT0207	Ig gamma chain C x
5	1156	50.8	377	2 A23511	Ig gamma-3 chain C
6	1154	50.7	377	2 A60764	Ig gamma-3 chain C
7	1148	50.5	326	1 G2HU	Ig gamma-2 chain C
8	1138.5	50.1	327	1 G4HU	Ig gamma-4 chain C
9	1134.5	49.9	289	1 G3HUM1	Ig gamma-3 heavy c
10	917	40.3	323	1 GHRB	Ig gamma chain C x
11	907	39.9	328	2 I47160	Ig gamma 2b chain
12	907	39.9	328	2 I47159	Ig gamma 2a chain
13	905	39.8	277	2 I47162	Ig gamma 4 chain C
14	895.5	39.4	329	1 G2GP	Ig gamma-2 chain C
15	891.5	39.2	328	2 I47158	Ig gamma 1 chain c
16	879	38.7	328	2 I47161	Ig gamma 3 chain c
17	858.5	37.8	470	2 S22080	Ig heavy chain pre
18	848.5	37.3	329	1 G3MSC	Ig gamma-3 chain C
19	842.5	37.0	328	1 G3MSM	Ig gamma-3 chain C
20	841	37.0	308	2 C30554	Ig heavy chain C x
21	841	37.0	422	2 S31459	Ig gamma-1 chain -
22	834	36.7	333	2 PS0018	Ig gamma-2b chain
23	822.5	36.2	444	2 PC4436	monoclonal antibod
24	817.5	35.9	326	2 PS0017	Ig gamma-1 chain C
25	812.5	35.7	324	1 G1MS	Ig gamma-1 chain C
26	812.5	35.7	393	1 G1MSM	Ig gamma-1 chain C
27	805	35.4	329	2 S00847	Ig gamma-2c chain
28	804	35.4	330	1 G2MSA	Ig gamma-2a chain
29	804	35.4	399	1 G2MSAM	Ig gamma-2a chain

30	804	35.4	469	2 S37483	Ig gamma-2a chain
31	797	35.0	335	1 G2MSAB	Ig gamma-2a chain
32	794	34.9	446	2 S40295	Ig gamma-2a chain
33	782	34.4	322	2 PS0019	Ig gamma-2a chain
34	779.5	34.3	405	1 G2MSBM	Ig gamma-2b chain
35	779.5	34.3	474	1 G2MS11	Ig gamma-2b chain
36	761	33.5	327	2 S06611	Ig gamma-2 chain C
37	757.5	33.3	475	2 S01321	Ig gamma-2b chain
38	702	30.9	180	2 I46732	Ig gamma heavy cha
39	574.5	25.3	218	2 A36040	Ig heavy chain V-1
40	572.5	25.2	249	2 S69340	Ig heavy chain VHI
41	566	24.9	152	2 S14236	Ig gamma-1 chain C
42	394.5	17.3	572	2 B46529	Ig Y heavy chain (
43	371	16.3	549	2 S04845	Ig heavy chain pre
44	366.5	16.1	388	1 EHMS	Ig epsilon chain C
45	365.5	16.1	453	2 S37768	Ig mu chain C regi

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: UNIPROT:P01857; EMBL:Z17370
A:Note: this sequence has the Gm(17) allotypic marker, 97-Lys, and the Gm(1) markers, 2
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: Protein
A:Residues: 1-96, R', 98-135 <CUN>
A:Note: this sequence has the Gm(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, 'E'
A:Note: this sequence has the Gm(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primaerstruktur

A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 272-330
A>Note: this sequence has the Gln(17) and Gln(11) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-36, 'K', 98-197, 'D', 199-238, 'E', 240, 'M', 242-366, 'D', 268-271, 'D', 273-330 <SCH
A>Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbrimide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kap
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:Keywords: Duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83, 144-204, 250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 54.1%; Score 1231; DB 1; Length 330;
Best Local Similarity 92.5%; Pred.No. 9.6e-68;
Matches 233; Conservative 3; Mismatches 12; Indels 4; Gaps 2;

Query Match 54.1%; Score 1231; DB 1; Length 330;
Best Local Similarity 92.5%;
Matches 233; Conservative 3; Mismatches 12; Indels

Qy	159	THDNICSGNSE-STOKCGIDV---TVDKTHTCCPCPAPELLGGPSVFLPPPKPKOTLMIS	214
Db	78	TOTYICNVNHPKSNTKVDKKVEPKSCDKTHTCCPCPAPELLGGPSVFLPPPKPKOTLMIS	137
Qy	215	RPPEVTCVVVDVSHEDPEVKENWVVDGVEVHNATKPREREQYNSTTRRVSVLTTLVHQDWL	274
Db	138	RPPEVTCVVVDVSHEDPEVKENWVVDGVEVHNATKPREREQYNSTTRRVSVLTTLVHQDWL	197
Qy	275	NGKEYKCKVSNKALPAPIEKTISAKAQPREPQYVTLPPSRDELTKNQVSLTCLVKGPYP	334
Db	198	NGKEYKCKVSNKALPAPIEKTISAKAQPREPQYVTLPPSRDELTKNQVSLTCLVKGPYP	257
Qy	335	SDIAVWESNGQPENNYKTTTPVLDSGGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHN	394
Db	258	SDIAVWESNGQPENNYKTTTPVLDSGGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHN	317
Qy	395	HYTKQSLSLSPG	406
Db	318	HYTKQSLSLSPG	329

RESULT 2

S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic

A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screening method for protein-protein interactions of cloned gene products
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PID:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match	54.0%;	Score 1228;	DB 4;	Length 255;
Best Local Similarity	100.0%;	Pred. NO. 1.1e-67;		
Matches 226;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	181	DXTHTCPCPAPELLGGPSVFLPPKPKDTMLSRTPETVCVVDSHEDPEVKNNWYD	240	
Db	29	DXTHTCPCPAPELLGGPSVFLPPKPKDTMLSRTPETVCVVDSHEDPEVKNNWYD	88	
QY	241	GVEVHNATKPREBQYNSYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAK	300	
Db	89	GVEVHNATKPREBQYNSYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAK	148	
QY	301	GQPREPQVYLLTPPRDELTKQVSLTCLVKGFYPSDIAVWESNGQENNNYKTTTPPVLDS	360	
Db	149	GQPREPQVYLLTPPRDELTKQVSLTCLVKGFYPSDIAVWESNGQENNNYKTTTPPVLDS	208	
QY	361	DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	406	
Db	209	DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	254	

RESULT 3

S69339
Ig heavy chain V region precursor - human
C/Species: Homo sapiens (man)
C/Date: 19-Mar-1997 #Sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C/Accession: S69339; S72664
R/Khamilichi, A.A.; Aoucuturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A/Rtitle: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A/Reference number: S69339; MUID:95262687; PMID:7744049

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-374 <KHA>
 A:Cross-references: EMBL:X81695
 R:Khamlichi, A.A.
 submitted to the EMBL Data Library, September 1994
 A:Reference number: S72664
 A:Accession: S72664
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-140,'C',142-374 <KH2>
 A:Cross-references: EMBL:X81695
 C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 53.8%; Score 1222.5; DB 2; Length 374;
Best Local Similarity 95.4%; Pred. No. 3.6e-67;
Matches 228; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

175	GIDVTV-----DKTHTCPCPAPELLGGSPSVFLPPPKPTLMISRTPEVTCVVVDVS	227
135	GTLVVTSSEKSCDKTHTCPCPAPELLGGSPSVFLPPPKPTLMISRTPEVTCVVVDVS	194
228	HEDPEVKFNKYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKA	287
195	HEDPEVKFNKYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKA	254

QY 288 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQP 347
 Db 255 LPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKQNQVSLTCLVKGFYPSDIAVWESNGQP 314
 QY 348 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPG 406
 Db 315 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPG 373

RESULT 4

PT0207
 Ig gamma chain C region - chimpanzee
 C:Species: Pan troglodytes (Chimpanzee)
 C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
 C:Accession: PT0207
 R: Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
 Mol. Immunol. 28, 319-322, 1991
 A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
 A:Reference number: PT0207; MUID:91287716; PMID:2062315
 A:Accession: PT0207
 A:Molecule type: mRNA
 A:Residues: 1-234 <EHR>
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 51.9%; Score 1180; DB 2; Length 234;
 Best Local Similarity 98.6%; Pred. No. 8.3e-65;
 Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 181 DKHTCTCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
 Db 15 DTHTCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 74
 QY 241 GVEVHNAKTPREEQNSTYRVVSVLTVLDHQLMNGKEYCKVKSNKALPAPIEKTISKAK 300
 Db 75 GVEVHNAKTPREEQNSTYRVVSVLTVLDHQLMNGKEYCKVKSNKALPAPIEKTISKAK 134
 QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQENNYKTTTPVLD 360
 Db 135 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQENNYKTTTPVLD 194
 QY 361 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKS 400
 Db 195 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKS 234

RESULT 5

A23511
 Ig gamma-3 chain C region (allotype G3m(b)) - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
 C:Accession: A23511
 R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
 Nucleic Acids Res. 14, 1779-1789, 1986
 A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cDNA
 A:Reference number: A23511; MUID:86148507; PMID:3081877
 A:Accession: A23511
 A:Molecule type: DNA
 A:Residues: 1-377 <HUC>
 A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
 C:Genetics:
 A:Gene: GDB:IGHG3
 A:Cross-references: GDB:119339; OMIM:147120
 A:Map position: 14q32.33-14q32.33
 A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.8%; Score 1156; DB 2; Length 377;
 Best Local Similarity 74.3%; Pred. No. 3.9e-63;
 Matches 223; Conservative 16; Mismatches 37; Indels 24; Gaps 4;

QY 110 VOAGTPERTNT--VCKRCPDGPFNSNETSKAP--CRKHTNCSVFGLLLTQKGNATHDNICSG 166
 Db 98 VELKTPGLDTHHTCPRCEP-KSCDTPPPCPCPEPKSCD----- 136
 QY 167 NSESTQKCGIDVTVDKTHCTCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDV 226
 Db 137 TTPPCPCPEPKSCDTPPPCPCPEPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDV 196
 QY 227 SHEDPEVKFNWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLDHQLMNGKEYCKVKSNK 286
 Db 197 SHEDPEVKFNWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLDHQLMNGKEYCKVKSNK 256
 QY 287 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ 346
 Db 257 ALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKQNQVSLTCLVKGFYPSDIAVWESNGQ 316
 QY 347 PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPG 406
 Db 317 PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPG 376

RESULT 6

A60764
 Ig gamma-3 chain C region, form LAT - human
 C:Species: Homo sapiens (man)
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
 C:Accession: A60764
 R:Huck, S.; Lefranc, G.; Lefranc, M.P.
 Immunogenetics 30, 250-257, 1989
 A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGH4 conversion
 A:Reference number: A60764; MUID:90007613; PMID:2571587
 A:Accession: A60764
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-377 <HUC>
 A:Cross-references: UNIPROT:Q8N4Y9
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.7%; Score 1154; DB 2; Length 377;
 Best Local Similarity 74.3%; Pred. No. 5.1e-63;
 Matches 223; Conservative 16; Mismatches 37; Indels 24; Gaps 4;

QY 110 VOAGTPERTNT--VCKRCPDGPFNSNETSKAP--CRKHTNCSVFGLLLTQKGNATHDNICSG 166
 Db 98 VELKTPGLDTHHTCPRCEP-KSCDTPPPCPCPEPKSCD----- 136
 QY 167 NSESTQKCGIDVTVDKTHCTCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDV 226
 Db 137 TTPPCPCPEPKSCDTPPPCPCPEPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDV 196
 QY 227 SHEDPEVKFNWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLDHQLMNGKEYCKVKSNK 286
 Db 197 SHEDPEVKFNWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLDHQLMNGKEYCKVKSNK 256
 QY 287 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ 346
 Db 257 ALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKQNQVSLTCLVKGFYPSDIAVWESNGQ 316
 QY 347 PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPG 406
 Db 317 PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPG 376

RESULT 7

G2HU
 Ig gamma-2 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
 C:Accession: A93906; A92809; A90752; A93132; A02148
 R:Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
 A>Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain c
 A:Reference number: A93906; MUID:82197621; PMID:6804948
 A:Accession: A93906
 A:Molecule type: DNA
 A:Residues: 1-326 <ELL>
 A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; F
 A:Note: Lys-326 is probably removed posttranslationally
 R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
 J. Immunol. 125, 1048-1054, 1980
 A>Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
 A:Reference number: A92809; MUID:81007873; PMID:6774012
 A:Contents: myeloma protein TII
 A:Accession: A92809
 A:Molecule type: protein
 A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
 A:Note: Trp-156 is at or near the complement-binding site
 R:Connell, G.E.; Parr, D.M.; Hofmann, T.
 Can. J. Biochem. 57, 758-767, 1979
 A>Title: The amino acid sequences of the three heavy chain constant region domains of a
 A:Reference number: A90752; MUID:80001357; PMID:113060
 A:Contents: myeloma protein Zie
 A:Accession: A90752
 A:Molecule type: protein
 A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
 A:Note: this sequence has since been revised
 R:Hofmann, T.; Parr, D.M.
 Mol. Immunol. 16, 923-925, 1979
 A>Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G
 A:Reference number: A93132; MUID:80114419; PMID:118920
 A:Contents: Zie
 A:Accession: A93132
 A:Molecule type: protein
 A:Residues: 238-275 <HOF>
 R:Hofmann, T.; Parr, D.M.
 submitted to the Atlas, March 1980
 A:Reference number: A94591
 A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
 A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
 ned
 R:Milstein, C.; Frangione, B.
 Biochem. J. 121, 217-225, 1971
 A>Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
 A:Reference number: A90253; MUID:72033500; PMID:4940472
 A:Contents: annotation; myeloma protein Sa, disulfide bonds
 R:Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A>Title: Structural studies of immunoglobulin G.
 A:Reference number: A93157; MUID:69064124; PMID:5782707
 A:Contents: annotation; Sa, disulfide bonds
 C:Genetics:
 A:Gene: GDB:IGHG2
 A:Cross-references: GDB:119338; OMIM:147110
 A:Map position: 14q32.33-14q32.33
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:133-202/Domain: immunoglobulin homology <IM2>
 F:239-306/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83, 140-200, 246-304/Disulfide bonds: #status experimental
 F:102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 50.5%; Score 1148; DB 1; Length 326;
 Best Local Similarity 87.0%; Pred. No. 1e-62;
 Matches 215; Conservative 9; Mismatches 11; Indels 12; Gaps 3;
 QY 171 TKCGID-----VTVDKT-----HTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEV 219
 DB 80 TYTCNVDPKPSNTKVDKTVKRCVCCVCPAPP-VAGPSVFLFPPKPKDTLMISRTPEV 138

QY 220 TCWVDVSHEDPVKFNWVVDGVVHNATKPREQYNSTYRVSVLTVLHODWLNKKEY 279
 DB 139 TCWVDVSHEDPEVQFNWVVDGVVHNATKPREQFNSTFRVSVLTVVHODWLNKKEY 198
 QY 280 KCKVSNKALPAPIETKISKAKQPREPQVYTLPPSRDELTKQVSLTCLVKGFYPSDIAV 339
 DB 199 KCKVSNKGLPAPIETKISKTKQPREPQVYTLPPSRDEWTKNOVSLTCLVKGFYPSDIAV 258
 QY 340 EWESNGQPNNTKTPPVLDSGSPFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQK 399
 DB 259 EWESNGQPNNTKTPPMLDSGSPFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQK 318
 QY 400 SLSLSFG 406
 DB 319 SLSLSFG 325
 RESULT 8
 G4HU
 IG gamma-4 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
 C:Accession: A90933; A90249; A02150
 R:Billison, J.; Buxbaum, J.; Hood, L.
 DNA 1, 11-18, 1981
 A>Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A:Reference number: A90933; MUID:83157104; PMID:6299662
 A:Accession: A90933
 A:Molecule type: DNA
 A:Residues: 1-327 <ELL>
 A:Cross-references: UNIPROT:P01861
 A:Note: the sequence was determined from the germline gene
 R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
 Biochem. J. 117, 33-47, 1970
 A>Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant re
 A:Reference number: A90249; MUID:70207560; PMID:4192699
 A:Accession: A90249
 A:Molecule type: protein
 A:Residues: 1-30; 81-326 <PIN>
 C:Genetics:
 A:Gene: GDB:IGHG4
 A:Cross-references: GDB:119340; OMIM:147130
 A:Map position: 14q32.33-14q32.33
 A:Introns: 99/1, 111/1, 221/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:99-110/Region: hinge
 F:134-203/Domain: immunoglobulin homology <IM2>
 F:240-307/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83, 141-201, 247-305/Disulfide bonds: #status predicted
 F:106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 50.1%; Score 1138.5; DB 1; Length 327;
 Best Local Similarity 71.1%; Pred. No. 3.8e-62;
 Matches 224; Conservative 16; Mismatches 30; Indels 45; Gaps 5;
 QY 137 APCRKHTN-----CSV-----FGLLLTKGNATHDNICSG 166
 DB 12 APCRSSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTV 71
 QY 167 NSPS-----TKCGID-----VTVDKT-----HTCPCPAPPELLGGPSVFLFPPKPKDTL 211
 DB 72 PSSSLGKTGTYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTL 131
 QY 212 MISRTPEVTCVVDVSHEDPEVKNWVVDGVVHNATKPREQYNSTYRVSVLTVLH 271
 DB 132 MISRTPEVTCVVDVSGEDPEVQFNWVVDGVVHNATKPREQFNSTYRVSVLTVLH 191

[illegible]

A;Note: this has the e15 allotypic marker, 185-Ala

Matches 170; Conservative 32; Mismatches 40; Indels 12; Gaps 5;
QY 165 SGNSESTQKGD-----VTVDK---THTCPPCP-APELLG-CPSPVLPFPKPKDTLMIS 214
DB 23 SLSLSKSYTCNVNHPATTTTKVDKRVGTTKPPCPICPACGPGPSAFIPFPKPKDTLMIS 82
QY 215 RPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 274
DB 83 RTPKVTCTCVVDVSGEPEVQFQSVYVDGVEVHTAQTAPKKEGQFNSTYRVVSVLPIQHODWL 142
QY 275 NGKEYKCKVSNKALPAPIETKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 334
DB 143 NGKEFKCKVNNKDLPAPIETRIISKAKGQTPREPQVYTLPPTEELSSKVTLTCLVGFYP 202
QY 335 SDIAVWESNGQ--PENNYKTPPVLDSGSGFFLYSKLTVDKSRWQGNFVSCSVNHEAL 392
DB 203 PDIDVWQRNGQPEPGNRYTTPQDDVDGTYFLYSKLAVDKASWQRGDTFOCAVNHAEAL 262
QY 393 HNHVTKSLSLSPG 406
DB 263 HNHVTKSIFKTPG 276

RESULT 14

G2GP

Ig gamma-2 chain C region - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 07-May-1981 #sequence revision 07-May-1981 #text change 09-Jul-2004

C;Accession: A94553; A90352; A90359; A90384; A90385; A02151

R;Trischmann, T.M.

submitted to the Atlas, April 1975

A;Reference number: A94553

A;Accession: A94553

A;Molecule type: protein

A;Residues: 1-3 <TRI>

A;Cross-references: UNIPROT:P01862

R;Birshstein, B.K.; Huseain, Q.Z.; Cebra, J.J.

Biochemistry 10, 18-25, 1971

A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am

A;Reference number: A90352; MUID:71058471; PMID:5538606

A;Accession: A90352

A;Molecule type: protein

A;Residues: 4-68

R;Turner, K.J.; Cebra, J.J.

Biochemistry 10, 9-17, 1971

A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am

A;Reference number: A90359; MUID:71058486; PMID:5538616

A;Accession: A90359

A;Molecule type: protein

A;Residues: 69-133;312-329 <TUR>

R;Tracey, D.E.; Cebra, J.J.

Biochemistry 13, 4796-4803, 1974

A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.

A;Reference number: A90384; MUID:75036072; PMID:4429665

A;Accession: A90384

A;Molecule type: protein

A;Residues: 134-226 <TRA>

R;Trischmann, T.M.; Cebra, J.J.

Biochemistry 13, 4804-4811, 1974

A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.

A;Reference number: A90385; MUID:75036073; PMID:4609467

A;Accession: A90385

A;Molecule type: protein

A;Residues: 227-311 <TR2>

R;Oliveira, B.; Lamm, M.E.

Biochemistry 10, 26-31, 1971

A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.

A;Reference number: A90354; MUID:71058474; PMID:4922544

A;Contents: annotation; disulfide bonds

A;Note: Cys-16 is involved in a heavy-light chain bond

A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds

C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;21-81/Domain: immunoglobulin homology <IM1>
F;135-204/Domain: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
F;142-202/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental

Query Match 39.4%; Score 895.5; DB 1; Length 329;

Best Local Similarity 59.7%; Pred. No. 2.1e-47;

Matches 173; Conservative 31; Mismatches 56; Indels 29; Gaps 5;

QY 127 GFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTVDKTH-- 184

DB 61 GLYSLTSMVTSPSSQKATC-----NVAHP-----ASSTK---VDKTVBPIRTP 100

QY 185 -----TCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 239

DB 101 ZBPBCTCPKCPPEENLGGPSVFLFPKPKDTLMISLTPTVTCVVVDVSDQDEPEVQTFWFV 160

QY 240 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKTISKA 299

DB 161 DNKPVGNATKPRVEQYNTTFRVESVLPQHODWLGKFKCKVYNKALPAPIETKTISKT 220

QY 300 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQP--ENNYKTPPV 357

DB 221 KGAPRMFVYTLPPSRDELTKSKSVVTCILINFFPADIHVEWASNRVPSVEKEYKNTPI 280

QY 358 LDSGSGFFLYSKLTVDKSRWQGNFVSCSVNHEALHNHVTQKSLSPG 406

DB 281 EDADGSYFLYSKLTVDKSAWDQGTVYTCVMEALHNHVTQKISRSPG 329

RESULT 15

I47158

Ig gamma 1 chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text change 21-Jan-2000

C;Accession: I47158

R;Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Accession: I47158

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-328 <KAC>

A;Cross-references: EMBL:U03778; NID:G433121; PIDN:AAA52216.1; PID:G433122

C;Genetics:

C;Gene: IgG1

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;133-202/Domain: immunoglobulin homology <IMW>

Query Match 39.2%; Score 891.5; DB 2; Length 328;

Best Local Similarity 59.7%; Pred. No. 3.6e-47;

Matches 172; Conservative 34; Mismatches 57; Indels 25; Gaps 4;

QY 125 PDGFFSNETSSKAPC-----RKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTV 180

DB 59 PSGLYSLSMVTVPASSLSKSYTCNV-----NHPATTTKVKRKGVI 100

QY 181 DKHTTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240

DB 101 HQPTCTPCGCE-VAGPSVFLFPKPKDTLMISQTPETVTCVVVDVSKHAEVQFQSWYVD 159

QY 241 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKTISKAK 300

DB 160 GVEVHTAETRPKEQFNSTYRVVSVLPIQHODWLGKFKCKVNNVNDLPAPITRTISKAI 219

QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTPPVVL 358

Db 220 GQREPVYTLPPPAEELSRKVTLCIVGFPPDIHVWKSNGQPEPENTYRTTTPQ 279
QY 359 DSDGSFFLYSKLTVDKSRWQGNVFSWHEALHNHYTKSLSPG 406
Db 280 DVDGTFFLYSKLAVDKARWDHGDKECAVMHEALHNHYTKSLTKQG 327

Search completed: March 8, 2005, 14:46:14
Job time : 17.5467 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:56 ; Search time 75.0656 Seconds

(without alignments)

2769.633 Million cell updates/sec

Title: US-09-389-782A-6

Perfect score: 2274

Sequence: 1 ETPPPKLYHDSHQLLC.....VMHEALHNHYTKSLSPG 406

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1231	54.1	330	1 GCI_HUMAN	P01857 homo sapien
2	1231	54.1	465	2 Q6GMX6	Q6gm66 homo sapien
3	1231	54.1	466	2 Q6IN78	Q6in78 homo sapien
4	1231	54.1	469	2 Q7Z7P5	Q7z7p5 homo sapien
5	1231	54.1	470	2 Q6PJA4	Q6pj44 homo sapien
6	1231	54.1	470	2 Q6ZJW1	Q6zjw1 homo sapien
7	1231	54.1	472	2 Q6N089	Q6n089 homo sapien
8	1231	54.1	475	2 Q6GMW7	Q6gmw7 homo sapien
9	1231	54.1	476	2 Q6GMX1	Q6gm61 homo sapien
10	1228	54.0	679	2 Q96PQ8	Q96pq8 homo sapien
11	1227	54.0	473	2 Q6P055	Q6p055 homo sapien
12	1227	54.0	475	2 Q6MZQ6	Q6mzq6 homo sapien
13	1227	54.0	480	2 Q6N094	Q6n094 homo sapien
14	1227	54.0	481	2 Q6N097	Q6n097 homo sapien
15	1227	54.0	482	2 Q7Z351	Q7z351 homo sapien
16	1225	53.9	348	2 Q6PYX1	Q6pyx1 homo sapien
17	1225	53.9	473	2 Q6MZV7	Q6mzv7 homo sapien
18	1225	53.9	478	2 Q6P181	Q6p181 homo sapien
19	1225	53.9	480	2 Q6PJF1	Q6pjf1 homo sapien
20	1225	53.9	544	2 Q6P095	Q6p095 homo sapien
21	1224	53.8	466	2 Q6N096	Q6n096 homo sapien
22	1220	53.6	475	2 Q6N095	Q6n095 homo sapien
23	1211	53.3	487	2 Q652L2	Q652l2 mus sp. fv/
24	1156	50.8	354	2 Q86T72	Q86tt2 homo sapien
25	1154	50.7	518	2 Q6N030	Q6n030 homo sapien
26	1152	50.7	521	2 Q8N4Y9	Q8n4y9 homo sapien
27	1148	50.5	326	1 GCI_HUMAN	P01859 homo sapien
28	1148	50.5	417	2 Q6N093	Q6n093 homo sapien
29	1147	50.4	464	2 Q6MZU6	Q6mzu6 homo sapien
30	1146	50.4	469	2 Q8NF17	Q8nfi7 homo sapien
31	1143	50.3	465	2 Q6P6C4	Q6p6c4 homo sapien

32	1138.5	50.1	327	1 GC4_HUMAN	P01861 homo sapien
33	1138.5	50.1	473	2 Q8TC63	Q8tc63 homo sapien
34	1134.5	49.9	290	1 GC3_HUMAN	P01860 homo sapien
35	1134	49.9	493	2 Q68CN4	Q68cn4 homo sapien
36	1130.5	49.7	476	2 Q6MZX7	Q6mzx7 homo sapien
37	1043	45.9	401	1 T11B_HUMAN	O00300 homo sapien
38	926.5	40.7	401	2 Q6P1I2	O6p1i2 mus musculus
39	922.5	40.6	401	1 T11B_MOUSE	O08712 mus musculus
40	917	40.3	323	1 GC_RABIT	P01870 coryctolagus
41	909	40.0	401	1 T11B_RAT	O08727 rattus norv
42	906	39.8	337	2 Q95M34	O95m34 equus cabal
43	895.5	39.4	329	1 Q52 CAVPO	P01862 cavia porce
44	851	37.4	470	2 Q7TMK1	Q7tmk1 mus musculus
45	848.5	37.3	329	1 GC3_MOUSE	P22436 mus musculus

ALIGNMENTS

RESULT 1

ID	GC1_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	23-OCT-2004 (Rel. 45, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	Name=IGHG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079 (1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170 (1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU)			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181 (1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.B., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			

RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RL Intrachain disulfide bonds.";
 RN Biochemistry 9:3188-3196(1970).
 RP [7]
 RX DISULFIDE BONDS.
 RA MEDLINE=77070267; PubMed=1002129;
 RE Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie). I: purification and
 RT characterization of the protein, the L- and H-chains, the cyanogen
 RT bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from *Staphylococcus*
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -1- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the
 CC GIM(3) marker and the GIM (non-1) markers.
 CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,
 CC 116, 198, 269 and 272.
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of
 CC residues 198, 267 and 272.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J00228; AAC92527.1; ALT_INIT.
 DR PIR; A93433; GHU.
 DR PDB; 1A77; X-ray; H=1-103.
 DR PDB; 1DSB; X-ray; B/H=1-101.
 DR PDB; 1D5I; X-ray; H=1-101.
 DR PDB; 1D6V; X-ray; H=1-101.
 DR PDB; 1DN2; X-ray; A/B=120-326.
 DR PDB; 1E4K; X-ray; A/B=106-329.
 DR PDB; 1FC1; X-ray; A/B=106-329.
 DR PDB; 1FC2; X-ray; D=106-329.
 DR PDB; 1FC3; X-ray; A=121-326.
 DR PDB; 1H2H; X-ray; H/K=1-330.
 DR PDB; 1I7Z; X-ray; B/D=1-103.
 DR PDB; 1IIS; X-ray; A/B=107-330.
 DR PDB; 1IIX; X-ray; A/B=107-330.
 DR PDB; 1L6X; X-ray; A=120-326.
 DR PDB; 1LQX; X-ray; A/B=119-330.
 DR PDB; 2RCS; X-ray; H=1-103.
 DR Genew; HGNC:5525; IGHG1.
 DR MiM; 147100; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW 3D-structure; Direct protein sequencing; Glycoprotein;
 KW Immunoglobulin C region; Immunoglobulin domain.
 FT NON TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 Hinge.

FT	DOMAIN	111	223	CH2.
FT	DISULFID	224	330	CH3.
FT	DISULFID	27	83	
FT	DISULFID	103	103	Interchain (with light chain).
FT	DISULFID	109	109	Interchain (with heavy chain).
FT	DISULFID	112	112	Interchain (with heavy chain).
FT	DISULFID	144	204	
FT	DISULFID	250	308	
FT	CARBOHYD	180	180	N-linked (GlcNAc. .).
FT	VARIANT	97	97	K -> R (in GIM(3) marker).
FT	VARIANT	239	239	/FTIG=VAR_003886.
FT	VARIANT	241	241	D -> E (in GIM(non-1) marker).
FT	VARIANT	241	241	/FTIG=VAR_003887.
FT	VARIANT	241	241	L -> M (in GIM(non-1) marker).
FT	VARIANT	241	241	/FTIG=VAR_003888.
FT	STRAND	23	24	
FT	STRAND	26	33	
FT	STRAND	38	38	
FT	STRAND	41	41	
FT	TURN	42	45	
FT	TURN	48	49	
FT	STRAND	50	52	
FT	STRAND	57	58	
FT	TURN	59	61	
FT	STRAND	62	71	
FT	HELEX	73	75	
FT	TURN	76	78	
FT	STRAND	82	87	
FT	TURN	88	91	
FT	STRAND	92	97	
FT	TURN	102	103	
FT	STRAND	122	126	
FT	HELEX	130	134	
FT	TURN	136	137	
FT	STRAND	141	149	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	167	
FT	STRAND	171	172	
FT	TURN	176	177	
FT	TURN	179	180	
FT	STRAND	183	190	
FT	HELEX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELEX	238	242	
FT	STRAND	245	256	
FT	STRAND	261	266	
FT	TURN	267	268	
FT	STRAND	269	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELEX	297	301	
FT	TURN	302	303	
FT	STRAND	306	311	
FT	TURN	313	314	
FT	HELEX	316	318	
FT	STRAND	319	324	
SQ	SEQUENCE	330 AA;	36106 MW;	3770EE106C2FA33D CRC64;

Query Match 54.1%; Score 1231; DB 1; Length 330;
 Best Local Similarity 92.5%; Pred. No. 1.4e-72;
 Matches 233; Conservative 3; Mismatches 12; Indels 4; Gaps 2;
 Qy 159 THDNICSGNSE-STQKCGIDV---TVDKTHTCPCPAPELLGGPSVFLPPPKDITMIS 214
 Db 78 TQTVICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPPKDITMIS 137

QY 215 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 274
 DB 138 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 197
 QY 275 NGKEYKCKVSNKALPAPIETKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFY 334
 DB 198 NGKEYKCKVSNKALPAPIETKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFY 257
 QY 335 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHN 394
 DB 258 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHN 317
 QY 395 HYTKSLSLSPG 406
 DB 318 HYTKSLSLSPG 329

RESULT 2
 Q6GMX6 PRELIMINARY; PRT; 465 AA.

AC Q6GMX6
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.S.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073766; AAH73766.1; -;
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00407; IG; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.

SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
 Query Match 54.1%; Score 1231; DB 2; Length 465;
 Best Local Similarity 92.5%; Pred. No. 2.1e-72;
 Matches 233; Conservative 3; Mismatches 12; Indels 4; Gaps 2;

QY 159 THDNICGNSH-STQKCGIDV---TVDKTHTCPCPAPELGPGSVLPFPKPKDTLMIS 214
 DB 213 TQTYICNVNKHPSNTKVDKVKVPKSCDKTHTCPCPAPELGPGSVLPFPKPKDTLMIS 272
 QY 215 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 274
 DB 273 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 332
 QY 275 NGKEYKCKVSNKALPAPIETKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFY 334
 DB 333 NGKEYKCKVSNKALPAPIETKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFY 392
 QY 335 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHN 394
 DB 393 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHN 452
 QY 395 HYTKSLSLSPG 406
 DB 453 HYTKSLSLSPG 464

RESULT 3
 Q6IN78 PRELIMINARY; PRT; 466 AA.

AC Q6IN78
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE IGHG1 protein.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.S.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC072419; AAH72419.1; -;
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.

RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018747; AAH18747.1; -
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 470 AA; 51715 MW; 7849556A11FD7D99 CRC64;
 Query Match 54.1%; Score 1231; DB 2; Length 470;
 Best Local Similarity 92.5%; Pred. No. 2.1e-72;
 Matches 233; Conservative 3; Mismatches 12; Indels 4; Gaps 2;
 QY 159 THDNICGNSG-STQKCGIDV---TVDKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 214
 DB 218 TQYICNVNHNKPSNTKVDKKEPKSCDKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 277
 QY 215 RTEPVTCTVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 274
 DB 278 RTEPVTCTVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 337
 QY 275 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 334
 DB 338 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 397
 QY 335 SDIAYEWESNGQPNKYKTPPVLDSGSPFLYSLKTVDKSRWQGNVFSCSVMHEALHN 394
 DB 398 SDIAYEWESNGQPNKYKTPPVLDSGSPFLYSLKTVDKSRWQGNVFSCSVMHEALHN 457
 QY 395 HYTKSLSLSPG 406
 DB 458 HYTKSLSLSPG 469
 RESULT 6
 Q725W1 PRELIMINARY; PRT; 470 AA.
 AC Q725W1
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.O., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC053984; AAH53984.1; -
 DR HSSP; P01857; IHZH.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
 Query Match 54.1%; Score 1231; DB 2; Length 470;
 Best Local Similarity 92.5%; Pred. No. 2.1e-72;
 Matches 233; Conservative 3; Mismatches 12; Indels 4; Gaps 2;
 QY 159 THDNICGNSG-STQKCGIDV---TVDKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 214
 DB 218 TQYICNVNHNKPSNTKVDKKEPKSCDKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 277
 QY 215 RTEPVTCTVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 274
 DB 278 RTEPVTCTVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 337
 QY 275 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 334
 DB 338 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 397
 QY 335 SDIAYEWESNGQPNKYKTPPVLDSGSPFLYSLKTVDKSRWQGNVFSCSVMHEALHN 394
 DB 398 SDIAYEWESNGQPNKYKTPPVLDSGSPFLYSLKTVDKSRWQGNVFSCSVMHEALHN 457
 QY 395 HYTKSLSLSPG 406
 DB 458 HYTKSLSLSPG 469
 RESULT 7
 Q6N089 PRELIMINARY; PRT; 472 AA.
 ID Q6N089
 AC Q6N089
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686P15220.
 GN Name=DKFZp686P15220;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RG The German Human cDNA Consortium;


```

Q6P055
ID Q6P055 PRELIMINARY; PRT; 473 AA.
AC Q6P055;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalko U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129857 CRC64;

Query Match 54.0%; Score 1227; DB 2; Length 473;
Best Local Similarity 92.1%; Pred. No. 3.9e-72;
Matches 232; Conservative 3; Mismatches 13; Indels 4; Gaps 2;

QY 159 THDNICSGNSE-STOKCGIDV---TVDKTHTCPCPAPELGGPSVFLPPKPKDTLMIS 214
Db 221 TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELGGPSVFLPPKPKDTLMIS 280

QY 215 RTPVETCVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVSVLTVLHQDWL 274
Db 281 RTPVETCVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVSVLTVLHQDWL 340

QY 275 NGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 334
Db 341 NGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 400

QY 335 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQOQGNVFCSCVMHEALHN 394

```

```

Db 401 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQOQGNVFCSCVMHEALHN 460
QY 395 HYTKQSLSLSPG 406
Db 461 HYTKQSLSLSPG 472

RESULT 12
Q6MZQ6 PRELIMINARY; PRT; 475 AA.
ID Q6MZQ6;
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DRFP686G11190.
GN Name=DRFP686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human CDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAA45972.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 54.0%; Score 1227; DB 2; Length 475;
Best Local Similarity 92.1%; Pred. No. 3.9e-72;
Matches 232; Conservative 3; Mismatches 13; Indels 4; Gaps 2;

QY 159 THDNICSGNSE-STOKCGIDV---TVDKTHTCPCPAPELGGPSVFLPPKPKDTLMIS 214
Db 223 TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELGGPSVFLPPKPKDTLMIS 282

QY 215 RTPVETCVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVSVLTVLHQDWL 274
Db 283 RTPVETCVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVSVLTVLHQDWL 342

QY 275 NGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 334
Db 343 NGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 402

QY 335 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQOQGNVFCSCVMHEALHN 394
Db 403 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQOQGNVFCSCVMHEALHN 462

QY 395 HYTKQSLSLSPG 406
Db 463 HYTKQSLSLSPG 474

RESULT 13
Q6N094 PRELIMINARY; PRT; 480 AA.
ID Q6N094
AC Q6N094;

```

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686O01196;
 GN Name=DKFZp686O01196;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RG The German Human cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640622; CAE45776.1; --
 DR HSSP; P01861; IADO.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG_2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00290; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein_
 SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;
 Query Match 54.0%; Score 1227; DB 2; Length 480;
 Best Local Similarity 92.1%; Pred. No. 4e-72;
 Matches 232; Conservative 3; Mismatches 13; Indels 4; Gaps 2;
 QY 159 THDNICSGNSE-STOKCGIDV---TVDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMIS 214
 DB 228 TQTYICNVNHNKPSNTKVDKKEPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMIS 287
 QY 215 RTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 274
 DB 288 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 347
 QY 275 NGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 334
 DB 348 NGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 407
 QY 335 SDIAVWESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQQGNVFSCSVMHEALHN 394
 DB 408 SDIAVWESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQQGNVFSCSVMHEGLHN 467
 QY 395 HYTKQSLSLSPG 406
 DB 468 HYTKQSLSLSPG 479
 RESULT 14
 Q6N097 PRELIMINARY; PRT; 481 AA.
 AC Q6N097;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein DKFZp686H20196;
 GN Name=DKFZp686H20196;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RG The German Human cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640622; CAE45776.1; --
 DR HSSP; P01861; IADO.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG_2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00290; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein_
 SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;
 Query Match 54.0%; Score 1227; DB 2; Length 480;
 Best Local Similarity 92.1%; Pred. No. 4e-72;
 Matches 232; Conservative 3; Mismatches 13; Indels 4; Gaps 2;
 QY 159 THDNICSGNSE-STOKCGIDV---TVDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMIS 214
 DB 228 TQTYICNVNHNKPSNTKVDKKEPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMIS 287
 QY 215 RTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 274
 DB 288 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 347
 QY 275 NGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 334
 DB 348 NGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 407
 QY 335 SDIAVWESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQQGNVFSCSVMHEALHN 394
 DB 408 SDIAVWESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQQGNVFSCSVMHEGLHN 467
 QY 395 HYTKQSLSLSPG 406
 DB 468 HYTKQSLSLSPG 479

RG The German Human cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640619; CAE45773.1; --
 DR HSSP; P01861; IADO.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG_2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00290; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein_
 SQ SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;
 Query Match 54.0%; Score 1227; DB 2; Length 481;
 Best Local Similarity 92.1%; Pred. No. 4e-72;
 Matches 232; Conservative 3; Mismatches 13; Indels 4; Gaps 2;
 QY 159 THDNICSGNSE-STOKCGIDV---TVDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMIS 214
 DB 229 TQTYICNVNHNKPSNTKVDKKEPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMIS 288
 QY 215 RTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 274
 DB 289 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWL 348
 QY 275 NGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 334
 DB 349 NGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 408
 QY 335 SDIAVWESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQQGNVFSCSVMHEALHN 394
 DB 409 SDIAVWESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQQGNVFSCSVMHEGLHN 468
 QY 395 HYTKQSLSLSPG 406
 DB 469 HYTKQSLSLSPG 480
 RESULT 15
 Q7Z351 PRELIMINARY; PRT; 482 AA.
 AC Q7Z351;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Hypothetical protein DKFZp686N02209;
 GN Name=DKFZp686N02209;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX538118; CAD98026.1; --
 DR HSSP; P01857; LHZH.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:11 ; Search time 84.7356 Seconds

(without alignments)
1843.986 Million cell updates/sec

Title: US-09-389-782A-7

Perfect score: 2264

Sequence: 1 EFTPPKYLHYDRETSQLLC.....VMHEALHNYTKSLSLSPG 404

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq19808:*

2: Geneseq19908:*

3: Geneseq20006:*

4: Geneseq20018:*

5: Geneseq20028:*

6: Geneseq20038:*

7: Geneseq20038b:*

8: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2264	100.0	404	AAB80903	Human OPG
2	2264	100.0	404	AAY72921	Human OPG
3	2199	97.1	425	ABG71831	Human OPG
4	2192.5	96.8	413	AAB80900	Human OPG
5	2192.5	96.8	413	AAY72918	Human OPG
6	2191.5	96.8	407	AAB80899	Human OPG
7	2191.5	96.8	407	AAY72917	Human OPG
8	2191	96.8	400	AAB80901	Human OPG
9	2191	96.8	400	AAY72919	Human OPG
10	2191	96.8	406	AAB80902	Human OPG
11	2191	96.8	406	AAY72920	Human OPG
12	2191	96.8	422	AAB66993	OPG-Fc. 4
13	1501.5	66.3	659	ABJ37103	Concatame
14	1501.5	66.3	659	ADQ79910	Human tum
15	1496.5	66.1	450	ADL06639	stnFR1:1
16	1496	66.1	489	ADM32913	Amino aci
17	1493.5	66.0	490	ABJ37099	Concatame
18	1493.5	66.0	490	ADQ79902	Human tum
19	1493.5	66.0	720	ABJ37101	Concatame
20	1493.5	66.0	720	ADQ79906	Human tum
21	1481	65.4	518	AAB50080	TNFR:Fc f
22	1481	65.4	518	AAB70001	stnFR (075
23	1467	64.8	518	2 AAR51003	Sequence
24	1460	64.5	485	2 AAR24016	Fusion pr
25	1436.5	63.4	444	5 ABG71833	RANK bind

ALIGNMENTS				
RESULT 1				
AAB80903				
ID	AAB80903	standard; protein; 404 AA.		
XX				
AC	AAB80903;			
XX				
DT	31-MAY-2001	(first entry)		
XX				
DE	Human OPG(22-194)-FcG10 fusion protein.			
XX				
KW	Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;			
KW	multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;			
KW	osteoclast formation inhibition; bone resorption inhibition;			
KW	immunoglobulin.			
XX				
OS	Homo sapiens.			
XX				
PN	WO200117543-A2.			
XX				
PD	15-MAR-2001.			
XX				
PF	18-AUG-2000; 2000WO-US022806.			
XX				
PR	03-SEP-1999; 99US-00389545.			
XX				
PA	(AMGE-) AMGEN INC.			
XX				
PI	Dunstan CR;			
XX				
DR	WPI; 2001-265936/27.			
XX				
PT	Preventing or treating lytic bone diseases, particularly associated with			
XX	cancer or metastasis, by administering an osteoprotegrin polypeptide.			
PS	Disclosure; Fig 7; 87pp; English.			
XX				
CC	The present invention relates to a method for the prevention or treatment			
CC	of lytic bone disease or multiple myeloma. Also the method can be used			
CC	for preventing metastasis of cancer to bone or osteosclerotic bone			
CC	metastasis. The method comprises administering an OPG (osteoprotegrin)			
CC	polypeptide or OPG fusion protein. The present sequence is one such OPG			
CC	fusion protein. OPG inhibits formation of osteoclasts (and thus bone			
CC	resorption) by blocking differentiation from monocytes/macrophage			
CC	precursors. The OPG polypeptide can be used in a method of preventing or			
CC	treating lytic bone disease, for preventing metastasis of cancer to bone			
CC	(e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,			
CC	rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal			
CC	tract, multiple myeloma or lymphoma) and preventing the osteosclerotic			

Abp58181	Human RAN
Aae34361	Human RAN
Adp3589	Herpes v1
Adp3589	Infection
Ado47876	Alpha-Her
Adb17001	Human RAN
Adb17002	Human RAN
Adb17000	Murine RA
Adj37102	Concatame
Adg79908	Human tum
Abj37098	Concatame
Adg79900	Human tum
Abj37100	Concatame
Adg79904	Human tum
Adl06637	stnFR1:19
Aaw60037	Antigenic
Adf57557	Mouse ymk
Abw02717	Mouse tm
Adj45758	Murine tm
Aaw50287	Human Fas

CC bone metastasis. The OPG fusion polypeptides are used in the prevention
 CC or treatment of loss of bone mass, which occurs in conditions including
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
 CC congenital forms of osteoporosis (osteogenesis imperfecta,
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
 CC hyperthyroidism and renal function disorders; osteopaenia following
 CC surgery, induced by steroid administration, and associated with disorders
 CC of the small and large intestine and with chronic hepatic and renal
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
 CC are also used in the replacement of structurally sound bone with
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
 CC in adults and juveniles; hyperparathyroidism, in congenital bone
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone
 CC metastases. The OPG fusion proteins can exhibit increased circulating
 CC half-lives and slower clearance times, thereby providing a more sustained
 CC activity. The OPG fusion protein comprises a fragment of the human OPG
 CC protein and the Fc region of immunoglobulin IgGammal (the hinge, CH2 and
 CC CH3 regions; see AAB80897-8)
 XX
 SQ Sequence 404 AA;

Query Match 100.0%; Score 2264; DB 4; Length 404;
 Best Local Similarity 100.0%; Pred. No. 3.2e-133;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ETPPKYLHYDEETSHQLLDCDKCPGTYLKQCTAKWTKVCAPCPDHYVYDTSWHTSDECL 60
 Db 1 ETPPKYLHYDEETSHQLLDCDKCPGTYLKQCTAKWTKVCAPCPDHYVYDTSWHTSDECL 60
 QY 61 YCSPVKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPPGFGVVGAGTPERNV 120
 Db 61 YCSPVKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPPGFGVVGAGTPERNV 120
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180
 Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180
 Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180
 QY 181 GGTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240
 Db 181 GGTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240
 QY 241 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQ 300
 Db 241 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQ 300
 QY 301 PREPQYVITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDG 360
 Db 301 PREPQYVITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDG 360
 QY 361 SPFLYSKLTVDKSRWQQGNVFCSVVMEALHNHYTKQSLSPG 404
 Db 361 SPFLYSKLTVDKSRWQQGNVFCSVVMEALHNHYTKQSLSPG 404

RESULT 2

AA72921
 ID AAY72921 standard; protein; 404 AA.

XX
 AC AAY72921;

XX
 DT 13-JUN-2001 (first entry)

XX
 DE Human OPG (22-194 residues)-FcG10 fusion protein.

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
 KW periodontal.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Region 1..173
 FT /note= "Derived from human osteoprotegerin fragment (22-
 FT 194 residues)"
 FT Region 174..182
 FT /label= Ser-(Gly) 8 linker
 FT Region 183..404
 FT /note= Corresponds to 10-231 residues of human IgG1 Fc
 FT region
 XX WO200118203-A1.
 PN
 XX 15-MAR-2001.
 PD
 XX 18-AUG-2000; 2000WO-US022797.
 PF
 XX 03-SEP-1999; 99US-00389782.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 PI Dunstan CR, Wooden SK, Mann MB;
 XX WPI; 2001-244572/25.
 DR
 XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
 PT by e.g. osteoporosis, Paget's disease and osteomyelitis.
 PS Claim 7; Fig 7; 119pp; English.
 XX
 CC The present sequence is a fusion protein comprising a sequence derived
 CC from human osteoprotegerin (OPG; 22-194 residues) which is fused with
 CC human immunoglobulin G1 (IgG1) FcG10 region (lacks 1-9 residues and has a
 CC Ser-(Gly) 8 linker). OPG negatively regulates the formation of osteoclasts
 CC in vitro and in vivo. It blocks the differentiation of osteoclasts from
 CC monocyte or macrophage precursors and the reabsorption of bone. The OPG-
 CC Fc fusion protein is administered for the treatment of bone loss
 CC resulting from osteoporosis, Paget's disease, osteomyelitis,
 CC hypercalcaemia, osteopenia associated with surgery or steroid
 CC administration, osteonecrosis, bone loss due to rheumatoid arthritis,
 CC periodontal bone loss, osteolytic metastasis and/or prosthetic loosening
 XX
 SQ Sequence 404 AA;
 Query Match 100.0%; Score 2264; DB 4; Length 404;
 Best Local Similarity 100.0%; Pred. No. 3.2e-133;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ETPPKYLHYDEETSHQLLDCDKCPGTYLKQCTAKWTKVCAPCPDHYVYDTSWHTSDECL 60
 Db 1 ETPPKYLHYDEETSHQLLDCDKCPGTYLKQCTAKWTKVCAPCPDHYVYDTSWHTSDECL 60
 QY 61 YCSPVKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPPGFGVVGAGTPERNV 120
 Db 61 YCSPVKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPPGFGVVGAGTPERNV 120
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180
 Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180
 QY 181 GGTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240
 Db 181 GGTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240
 QY 241 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQ 300

Db 241 EVHNAKTKPREQYNSYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQ 300
QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 360
Db 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 360
QY 361 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 404
Db 361 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 404

RESULT 3

ABG71831
ID ABG71831 standard; protein; 425 AA.

XX AC ABG71831;

XX DT 14-APR-2003 (first entry)

XX DE Human OPG protein for expression in mammalian cells.

XX KW RANKL; human receptor activator of NfkappaB; osteoprotegerin; OPG;
KW RANKL ligand; osteoclastogenesis; osteoclast inhibitor; gene therapy;
KW osteoporosis; bone disease; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200264782-A2.

XX PD 22-AUG-2002.

XX PF 08-FEB-2002; 2002WO-DK000090.

XX PR 09-FEB-2001; 2001DK-00000214.

XX PR 09-FEB-2001; 2001US-0267843P.

XX PR 23-MAR-2001; 2001DK-00000498.

XX PR 23-MAR-2001; 2001US-0278320P.

XX PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX PI Haaning JM, Halkier T;

XX DR WPI; 2002-691592/74.

XX DR N-PSDB; ABS56347.

XX PT Novel human receptor activator of NfkappaB (hRANK) or human
PT osteoprotegerin (hOPG) variant polypeptides which bind to RANK ligand
PT (RANKL) with equivalent binding affinity as hRANK or hOPG, useful for
PT treating osteoporosis.

XX PS Example 4; Fig 12; 129pp; English.

XX CC This invention relates to a novel polypeptide having an amino acid
CC sequence that is different from and is at least about 70% identical to
CC the amino acid sequence of human receptor activator of NfkappaB (hRANK)
CC or human osteoprotegerin (hOPG), and which has a binding affinity to RANK
CC ligand (RANKL) that is at least as high as the binding affinity of hRANK
CC or hOPG to RANKL, as determined by functional competition assay. The
CC protein of the invention may have osteopathic activity and may act as a
CC RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclast activity
CC inhibitor. The nucleotide sequence shown in the invention may be used in
CC gene therapy. The protein of the invention or fusion proteins comprising
CC this protein are useful as a pharmaceutical, and in the preparation of a
CC medicament for treating or preventing osteoporosis, or other bone
CC diseases or diseases associated with binding of RANKL to the RANK
CC receptor. A host cell containing a vector expressing the protein is
CC useful for producing a polypeptide having binding affinity to RANKL,
CC where the polypeptide comprises at least one N- or O-glycosylation site
CC and the host cell is a eukaryotic host cell capable of in vivo
CC glycosylation, and/or the polypeptide is subjected to conjugation to a
CC non-polypeptide moiety in vitro. The protein of the invention has

CC increased functional in vivo half-life and/or serum half-life compared to
CC hRANK or hOPG and has an improved binding affinity to RANKL compared to
CC the binding affinity of hRANK or hOPG to RANKL, as determined by a
CC functional competition assay. The present sequence represents a human OPG
CC protein modified for expression in a mammalian system, this sequence has
CC the human OPG protein fused to a Leu-Glu dipeptide and amino acid
CC residues 247-475 of human IgG1

XX SQ Sequence 425 AA;

Query Match 97.1%; Score 2199; DB 5; Length 425;
Best Local Similarity 97.8%; Pred. No. 3.9e-129;
Matches 395; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDETSQQLCDKPPGTYLKQHTAKWTKVCAPCPDHYTDSWHTSDECL 60

Db 22 ETFPKYLHYDETSQQLCDKPPGTYLKQHTAKWTKVCAPCPDHYTDSWHTSDECL 81

QY 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSPPGFGVVQAGTPERNTV 120

Db 82 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSPPGFGVVQAGTPERNTV 141

QY 121 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQKSGGGGG 180

Db 142 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQKLEKSSDK 201

QY 181 GGTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPPVKNNWYVDGV 240

Db 202 THTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPPVKNNWYVDGV 261

QY 241 EVHNAKTKPREQYNSYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQ 300

Db 262 EVHNAKTKPREQYNSYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQ 321

QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 360

Db 322 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 381

QY 361 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 404

Db 382 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 425

RESULT 4

AAB80900

ID AAB80900 standard; protein; 413 AA.

XX AC AAB80900;

XX DT 31-MAY-2001 (first entry)

XX DE Human OPG(22-201)-Fc fusion protein.

XX KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegerin;
KW osteoclast formation inhibition; bone resorption inhibition;
KW immunoglobulin.

XX OS Homo sapiens.

XX PN WO200117543-A2.

XX PD 15-MAR-2001.

XX PF 18-AUG-2000; 2000WO-US022806.

XX PR 03-SEP-1999; 99US-00389545.

XX PA (AMGE-) AMGEN INC.

XX PI Dunstan CR;

XX DR WPI; 2001-265936/27.

XX Preventing or treating lytic bone diseases, particularly associated with
PT cancer or metastasis, by administering an osteoprotegerin polypeptide.
XX
XX Disclosure; Fig 4; 87pp; English.
XX
XX The present invention relates to a method for the prevention or treatment
CC of lytic bone disease or multiple myeloma. Also the method can be used
CC for preventing metastasis of cancer to bone or osteosclerotic bone
CC metastasis. The method comprises administering an OPG (osteoprotegerin)
CC polypeptide or OPG fusion protein. The present sequence is one such OPG
CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone
CC resorption) by blocking differentiation from monocytes/macrophage
CC precursors. The OPG polypeptide can be used in a method of preventing or
CC treating lytic bone disease, for preventing metastasis of cancer to bone
CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic
CC bone metastasis. The OPG fusion polypeptides are used in the prevention
CC or treatment of loss of bone mass, which occurs in conditions including
CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
CC congenital forms of osteoporosis (osteogenesis imperfecta,
CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
CC due to immobilisation of extremities; Paget's disease of bone (osteitis
CC deformans) in adults and juveniles; osteomyelitis, or an infectious
CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
CC leukaemia); idiopathic hypercalcaemia, and hypercalcaemia associated with
CC hyperthyroidism and renal function disorders; osteopaenia following
CC surgery, induced by steroid administration, and associated with disorders
CC of the small and large intestine and with chronic hepatic and renal
CC diseases; osteonecrosis, or bone cell death, associated with traumatic
CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
CC cell anaemia, systemic lupus erythematosus and other conditions; bone
CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
CC are also used in the replacement of structurally sound bone with
CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
CC in adults and juveniles; hyperparathyroidism, in congenital bone
CC disorders such as fibrous dysplasia, and in osteosclerotic bone
CC metastases. The OPG fusion proteins can exhibit increased circulating
CC half-lives and slower clearance times, thereby providing a more sustained
CC activity. The OPG fusion protein comprises a fragment of the human OPG
CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and
CC CH3 regions; see AAB80897-8)
XX
XX Sequence 413 AA;

Query Match 96.8%; Score 2192.5; DB 4; Length 413;
Best Local Similarity 95.9%; Pred. No. 9,6e-129;
Matches 396; Conservative 0; Mismatches 8; Indels 9; Gaps 1;
QY 1 ETTPPKYLHYDETSKLLCDKCPGTYLKQCHTAKWTKVTCAPCPHYHYTDSWHTSDECL 60
Db 1 ETTPPKYLHYDETSKLLCDKCPGTYLKQCHTAKWTKVTCAPCPHYHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVKQECNTRHNRCVCEKGRYLEIEFCLKHSRCPGFGVQAGTPERNTV 120
Db 61 YCSPVCKELQYVKQECNTRHNRCVCEKGRYLEIEFCLKHSRCPGFGVQAGTPERNTV 120
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSSTQKSGGGGG 180
Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSSTQKCGIDVTA 180
QY 181 GG-----TCPCPAPELGGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEV 231
Db 181 AAPKSCDKTHTCPCPAPELGGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEV 240
QY 232 KFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIE 291
Db 241 KFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIE 300

QY 292 KTIISKAKGPRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 351
Db 301 KTIISKAKGPRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 360
QY 352 TTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSVHVEALHNNHYTKQSLSPG 404
Db 361 TTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSVHVEALHNNHYTKQSLSPG 413
RESULT 5
AA72918
ID AAY72918 standard; protein; 413 AA.
XX
AC AAY72918;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human osteoprotegerin (22-201 residues)-IgG1 Fc region fusion protein.
XX
KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
KW periodontal.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..179
FT /note= "derived from human osteoprotegerin fragment (22-
FT 201 residues)"
FT Region 180..182
FT /label= Linker
FT Region 183..413
FT /label= Human_IgG1_Fc_region
XX
PN WO200118203-A1.
XX
PD 15-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-US022797.
XX
PR 03-SEP-1999; 99US-00389782.
XX (AMGE-) AMGEN INC.
XX Dunstan CR, Wooden SK, Mann MB;
XX
DR WPI; 2001-244572/25.
XX
PT Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
PT by e.g. osteoporosis, Paget's disease and osteomyelitis.
XX
PS Example 1; Fig 4; 119pp; English.
XX
CC The present sequence is a fusion protein comprising a sequence derived
CC from human osteoprotegerin (OPG; 22-201 residues) which is fused with
CC human immunoglobulin G1 (IgG1) Fc region by a linker. OPG negatively
CC regulates the formation of osteoclasts in vitro and in vivo. It blocks
CC the differentiation of osteoclasts from monocyte or macrophage precursors
CC and the reabsorption of bone. The OPG-Fc fusion protein is administered
CC for the treatment of bone loss resulting from osteoporosis, Paget's
CC disease, osteomyelitis, hypercalcaemia, osteopenia associated with
CC surgery or steroid administration, osteonecrosis, bone loss due to
CC rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or
CC prosthetic loosening
XX
SQ Sequence 413 AA;

Query Match 96.8%; Score 2192.5; DB 4; Length 413;
Best Local Similarity 95.9%; Pred. No. 9,6e-129;
Matches 396; Conservative 0; Mismatches 8; Indels 9; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 DB 1 ETTPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVQAGTPERTV 120
 DB 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVQAGTPERTV 120
 QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKSGGGG 180
 DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKSGGGG 180
 QY 181 GG-----TCPPCAPPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEV 231
 DB 181 AAPKSCDKTHTCPPCAPPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEV 240
 QY 232 KFNWYDGVVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 291
 DB 241 KFNWYDGVVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 300
 QY 292 KTISKAKQPREQVYTLPPSRDELTKQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 351
 DB 301 KTISKAKQPREQVYTLPPSRDELTKQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 360
 QY 352 TTPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 404
 DB 361 TTPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 413

RESULT 6

AAB80899
 ID AAB80899 standard; protein; 407 AA.

XX AC AAB80899;
 XX AC
 XX 31-MAY-2001 (first entry)
 XX Human OPG(22-194)-Fc fusion protein.
 XX Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
 KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
 KW osteoclast formation inhibition; bone resorption inhibition;
 KW immunoglobulin.
 XX Homo sapiens.
 XX WO200117543-A2.
 XX 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-US022806.
 XX 03-SEP-1999; 99US-00389545.
 XX (AMGE-) AMGEN INC.
 XX Dunstan CR;
 XX WPI; 2001-265936/27.
 XX Preventing or treating lytic bone diseases, particularly associated with
 PT cancer or metastasis, by administering an osteoprotegrin polypeptide.
 XX Disclosure; Fig 3; 87pp; English.
 XX The present invention relates to a method for the prevention or treatment
 CC of lytic bone disease or multiple myeloma. Also the method can be used
 CC for preventing metastasis of cancer to bone or osteosclerotic bone
 CC metastasis. The method comprises administering an OPG (osteoprotegrin)
 CC polypeptide or OPG fusion protein. The present sequence is one such OPG
 CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone
 CC resorption) by blocking differentiation from monocytes/macrophage
 CC precursors. The OPG polypeptide can be used in a method of preventing or

CC treating lytic bone disease, for preventing metastasis of cancer to bone
 CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
 CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
 CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic
 CC bone metastasis. The OPG fusion polypeptides are used in the prevention
 CC or treatment of loss of bone mass, which occurs in conditions including
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
 CC congenital forms of osteoporosis (osteogenesis imperfecta,
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
 CC hyperthyroidism and renal function disorders; osteopaenia following
 CC surgery, induced by steroid administration, and associated with disorders
 CC of the small and large intestine and with chronic hepatic and renal
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
 CC are also used in the replacement of structurally sound bone with
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
 CC in adults and juveniles; hyperparathyroidism, in congenital bone
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone
 CC metastases. The OPG fusion proteins can exhibit increased circulating
 CC half-lives and slower clearance times, thereby providing a more sustained
 CC activity. The OPG fusion protein comprises a fragment of the human OPG
 CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and
 CC CH3 regions; see AAB80897-8)

XX SQ Sequence 407 AA;

Query Match 96.8%; Score 2191.5; DB 4; Length 407;
 Best Local Similarity 97.1%; Pred. No. 1.1e-128;
 Matches 395; Conservative 1; Mismatches 8; Indels 3; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 DB 1 ETTPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVQAGTPERTV 120
 DB 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVQAGTPERTV 120
 QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKSGG--G 177
 DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKAAEPPKS 180
 QY 178 GGGGGTCTPPCAPPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 237
 DB 181 CDKTHCTCPCAPPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 240
 QY 238 DGVVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 297
 DB 241 DGVVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 300
 QY 298 KGQPREQVYTLPPSRDELTKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLVD 357
 DB 301 KGQPREQVYTLPPSRDELTKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLVD 360
 QY 358 SDGSFPLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 404
 DB 361 SDGSFPLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 407

RESULT 7

AAY72917
 ID AAY72917 standard; protein; 407 AA.

XX AAY72917;
 AC AAY72917;

XX DT 13-JUN-2001 (first entry)

XX DE Human osteoprotegerin (22-194 residues) - IgG1 Fc region fusion protein.

XX KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

XX KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;

XX KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;

XX KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;

XX KW periodontal.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 1. .173

XX FT /notes= "Derived from human osteoprotegerin fragment (22-194 residues)"

XX FT 174. .176

XX FT /label= Linker

XX FT 177. .407

XX FT /label= Human_IgG1_Fc_region

XX PN WO200118203-A1.

XX PN 15-MAR-2001.

XX PF 18-AUG-2000; 2000WO-US022797.

XX PR 03-SEP-1999; 99US-00389782.

XX PA (AMGE-) AMGEN INC.

XX PI Dunstan CR, Wooden SK, Mann MB;

XX DR WPI; 2001-244572/25.

XX PT Osteoprotegerin-Fc protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis.

XX PS Example 1; Fig 3; 119pp; English.

XX CC The present sequence is a fusion protein comprising a sequence derived from human osteoprotegerin (OPG; 22-194 residues) which is fused with human immunoglobulin G1 (IgG1) Fc region by a linker. OPG negatively regulates the formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion protein is administered for the treatment of bone loss resulting from osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia associated with surgery or steroid administration, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic loosening

XX SQ Sequence 407 AA;

Query Match 96.8%; Score 2191.5; DB 4; Length 407;

Best Local Similarity 97.1%; Pred. No. 1.1e-128;

Matches 395; Conservative 1; Mismatches 8; Indels 3; Gaps 1;

QY 1 ETFFPKYLYHDETSHTQLLDCRCPGTYLKHQCTAKWTKVACPCPDHYVTSWHTSDCL 60

DB 1 ETFFPKYLYHDETSHTQLLDCRCPGTYLKHQCTAKWTKVACPCPDHYVTSWHTSDCL 60

QY 61 YCSPVCKELQYVKQECNRTHNRVCEKGRYLIIEFCLKHRSCTPGFGVQAGTPERNV 120

DB 61 YCSPVCKELQYVKQECNRTHNRVCEKGRYLIIEFCLKHRSCTPGFGVQAGTPERNV 120

QY 121 CKRCPDGFPSNTSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESQKSGG---G 177

DB 121 CKRCPDGFPSNTSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESQKAAEPKS 180

QY 178 GGGGTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 237

DB 181 CDKTHTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 240

QY 238 DGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKA 297

DB 241 DGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKA 300

QY 298 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 357

DB 301 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360

QY 358 SDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 404

DB 361 SDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 407

RESULT 8

AAB80301

ID AAB80901 standard; protein; 400 AA.

XX AC AAB80901;

XX DT 31-MAY-2001 (first entry)

XX DE Human OPG(22-194)-FcdeltaC fusion protein.

XX KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;

XX KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegerin;

XX KW osteoclast formation inhibition; bone resorption inhibition;

XX KW immunoglobulin.

XX OS Homo sapiens.

XX PN WO200117543-A2.

XX PD 15-MAR-2001.

XX PF 18-AUG-2000; 2000WO-US022806.

XX PR 03-SEP-1999; 99US-00389545.

XX PA (AMGE-) AMGEN INC.

XX PI Dunstan CR;

XX DR WPI; 2001-265936/27.

XX PT Preventing or treating lytic bone diseases, particularly associated with cancer or metastasis, by administering an osteoprotegerin polypeptide.

XX PS Claim 11; Fig 5; 87pp; English.

CC The present invention relates to a method for the prevention or treatment of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegerin) polypeptide or OPG fusion protein. The present sequence is one such OPG fusion protein. OPG inhibits formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The OPG polypeptide can be used in a method of preventing or treating lytic bone disease, for preventing metastasis of cancer to bone (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal, rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal tract, multiple myeloma or lymphoma) and preventing the osteosclerotic bone metastasis. The OPG fusion polypeptides are used in the prevention or treatment of loss of bone mass, which occurs in conditions including osteoporosis, such as primary osteoporosis, endocrine osteoporosis (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and congenital forms of osteoporosis (osteogenesis imperfecta, homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis due to immobilisation of extremities; Paget's disease of bone (osteitis deformans) in adults and juveniles; osteomyelitis, or an infectious lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung and kidney) and haematologic malignancies (multiple myeloma, lymphoma and

CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
 CC hyperthyroidism and renal function disorders; osteopaenia following
 CC surgery, induced by steroid administration, and associated with disorders
 CC of the small and large intestine and with chronic hepatic and renal
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
 CC are also used in the replacement of structurally sound bone with
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
 CC in adults and juveniles; hyperparathyroidism, in congenital bone
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone
 CC metastases. The OPG fusion proteins can exhibit increased circulating
 CC half-lives and slower clearance times, thereby providing a more sustained
 CC activity. The OPG fusion protein comprises a fragment of the human OPG
 CC protein and the FC region of immunoglobulin IgGgamma1 (the hinge, CH2 and
 CC CH3 regions; see AAB80897-8)
 XX
 SQ Sequence 400 AA;

Query Match 96.8%; Score 2191; DB 4; Length 400;
 Best Local Similarity 97.8%; Pred. No. 1.1e-128;
 Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

QY 1 ETPPPKYLHYDEBTSQQLCDKCPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 60
 DB 1 ETPPPKYLHYDEBTSQQLCDKCPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVCKELQYVQECNTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGWAGTTPERTV 120
 DB 61 YCSPVCKELQYVQECNTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGWAGTTPERTV 120
 QY 121 CKRCPDGFFNETSSKAPCRKHTNCSVFGLLLTKGNATHDNCNSENSTOKSGGGGG 180
 DB 121 CKRCPDGFFNETSSKAPCRKHTNCSVFGLLLTKGNATHDNCNSENSTOKV----DK 176
 QY 181 GGTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGV 240
 DB 177 THTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGV 236
 QY 241 EVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 300
 DB 237 EVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 296
 QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 360
 DB 297 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 356
 QY 361 SPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 404
 DB 357 SPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 400

RESULT 9
 AAY72919
 ID AAY72919 standard; protein; 400 AA.
 XX
 AC AAY72919;
 XX
 XX
 DT 13-JUN-2001 (first entry)
 XX
 DE Human OPG (22-194 aa)-Fc region (lacking 1-5 residues) fusion protein.
 XX
 KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
 KW periodontal.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers

FT Region 1..173 /note= "Derived from human osteoprotegerin fragment (22-
 FT Region 174 /label= Linker
 FT Region 175..400 /note= Human IgG1 Fc region lacking 1-5 residues
 XX WO200118203-A1.
 PN 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-US022797.
 XX 03-SEP-1999; 99US-00389782.
 PR (AMGE-) AMGEN INC.
 XX Dunstan CR, Wooden SK, Mann MB;
 XX WPI; 2001-244572/25.
 DR Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
 XX by e.g. osteoporosis, Paget's disease and osteomyelitis.
 PS Claim 7; Fig 5; 119pp; English.
 XX The present sequence is a fusion protein comprising a sequence derived
 CC from human osteoprotegerin (OPG; 22-194 residues) which is fused with
 CC human immunoglobulin G1 (IgG1) Fc region lacking 1-5 residues by a
 CC linker. OPG negatively regulates the formation of osteoclasts in vitro
 CC and in vivo. It blocks the differentiation of osteoclasts from monocyte
 CC or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion
 CC protein is administered for the treatment of bone loss resulting from
 CC osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia
 CC associated with surgery or steroid administration, osteonecrosis, bone
 CC loss due to rheumatoid arthritis, periodontal bone loss, osteolytic
 CC metastasis and/or prosthetic loosening
 XX
 SQ Sequence 400 AA;

Query Match 96.8%; Score 2191; DB 4; Length 400;
 Best Local Similarity 97.8%; Pred. No. 1.1e-128;
 Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;
 QY 1 ETPPPKYLHYDEBTSQQLCDKCPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 60
 DB 1 ETPPPKYLHYDEBTSQQLCDKCPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVCKELQYVQECNTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGWAGTTPERTV 120
 DB 61 YCSPVCKELQYVQECNTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGWAGTTPERTV 120
 QY 121 CKRCPDGFFNETSSKAPCRKHTNCSVFGLLLTKGNATHDNCNSENSTOKSGGGGG 180
 DB 121 CKRCPDGFFNETSSKAPCRKHTNCSVFGLLLTKGNATHDNCNSENSTOKV----DK 176
 QY 181 GGTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGV 240
 DB 177 THTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGV 236
 QY 241 EVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 300
 DB 237 EVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 296
 QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 360
 DB 297 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 356
 QY 361 SPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 404
 DB 357 SPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 400

RESULT 10
 AAB80902
 ID AAB80902 standard; protein; 406 AA.
 XX
 AC AAB80902;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human OPG(22-201)-FcDeltaC fusion protein.
 XX
 KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
 KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegerin;
 KW osteoclast formation inhibition; bone resorption inhibition;
 KW immunoglobulin.
 XX
 OS Homo sapiens.
 XX
 PN WO200117543-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-US022806.
 XX
 PR 03-SEP-1999; 99US-00389545.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Dunstan CR;
 XX
 DR WPI; 2001-265936/27.
 XX
 XX Preventing or treating lytic bone diseases, particularly associated with
 PT cancer or metastasis, by administering an osteoprotegerin polypeptide.
 XX
 PS Disclosure; Fig 6; 87pp; English.
 XX
 CC The present invention relates to a method for the prevention or treatment
 CC of lytic bone disease or multiple myeloma. Also the method can be used
 CC for preventing metastasis of cancer to bone or osteosclerotic bone
 CC metastasis. The method comprises administering an OPG (osteoprotegerin)
 CC polypeptide or OPG fusion protein. The present sequence is one such OPG
 CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone
 CC resorption) by blocking differentiation from monocytes/macrophage
 CC precursors. The OPG polypeptide can be used in a method of preventing or
 CC treating lytic bone disease, for preventing metastasis of cancer to bone
 CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
 CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
 CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic
 CC bone metastasis. The OPG fusion polypeptides are used in the prevention
 CC or treatment of loss of bone mass, which occurs in conditions including
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
 CC congenital forms of osteoporosis (osteogenesis imperfecta,
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
 CC hyperthyroidism and renal function disorders; osteopaenia following
 CC surgery, induced by steroid administration, and associated with disorders
 CC of the small and large intestine and with chronic hepatic and renal
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
 CC are also used in the replacement of structurally sound bone with
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
 CC in adults and juveniles; hyperparathyroidism, in congenital bone
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone
 CC metastases. The OPG fusion proteins can exhibit increased circulating

CC half-lives and slower clearance times, thereby providing a more sustained
 CC activity. The OPG fusion protein comprises a fragment of the human OPG
 CC protein and the Fc region of immunoglobulin IgGammal (the hinge, CH2 and
 CC CH3 regions; see AAB80897-8)
 XX
 SQ Sequence 406 AA;

Query Match 96.8%; Score 2191; DB 4; Length 406;
 Best Local Similarity 97.5%; Pred. No. 1.2e-128;
 Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;
 QY 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQHTAKWTKVACPCPDHYTDSWHTSDECL 60
 DB 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQHTAKWTKVACPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVKELQYVKQECNTHNRVCEKGRVLEIEFCLKHSRCPGFGVQAGTPTNTV 120
 DB 61 YCSPVKELQYVKQECNTHNRVCEKGRVLEIEFCLKHSRCPGFGVQAGTPTNTV 120
 QY 121 CKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKSG- -GGG 178
 DB 121 CKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKSG- -GGG 178
 QY 179 GGGTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 238
 DB 181 DKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
 QY 239 GVEVNAKTKPREQYNSTYRVSVLTVLDHDLNGKEYCKVSNKALPAPIETISKAK 298
 DB 241 GVEVNAKTKPREQYNSTYRVSVLTVLDHDLNGKEYCKVSNKALPAPIETISKAK 300
 QY 299 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 358
 DB 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 360
 QY 359 DGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 404
 DB 361 DGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 406

RESULT 11

AA772920
 ID AA772920 standard; protein; 406 AA.

AC AA772920;
 XX

DT 13-JUN-2001 (first entry)
 XX

DE Human OPG (22-201 aa)-Fc region (lacking 1-5 residues) fusion protein.
 XX

KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
 KW hypercalcaemia; osteopaenia; osteonecrosis; rheumatoid arthritis;
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
 KW periodontal.
 XX

OS Homo sapiens.
 XX

PH Key Location/Qualifiers
 XX

FT Region 1..179
 FT /note= "Derived from human osteoprotegerin fragment (22-
 FT 201 residues)"
 FT 180
 FT Region /label= Linker
 FT 181..406
 FT /note= Human IgG1 Fc region lacking 1-5 residues;
 FT (Corresponds to 6-231 residues of IgG1 Fc region)
 XX

PN WO200118203-A1.
 XX

PD 15-MAR-2001.
 XX

PF 18-AUG-2000; 2000WO-US022797.
 XX

XX 03-SEP-1999; 99US-00389782.
 XX (AMGE-) AMGEN INC.
 XX Dunstan CR, Wooden SK, Mann MB;
 XX WPI, 2001-244572/25.
 XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
 XX by e.g. osteoporosis, Paget's disease and osteomyelitis.
 XX Claim 7; Fig 6; 119pp; English.
 XX The present sequence is a fusion protein comprising a sequence derived
 XX from human osteoprotegerin (OPG; 22-201 residues) which is fused with
 XX human immunoglobulin G1 (IgG1) Fc region lacking 1-5 residues, by a
 XX linker. OPG negatively regulates the formation of osteoclasts in vitro
 XX and in vivo. It blocks the differentiation of osteoclasts from monocyte
 XX or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion
 XX protein is administered for the treatment of bone loss resulting from
 XX osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia
 XX associated with surgery or steroid administration, osteonecrosis, bone
 XX loss due to rheumatoid arthritis, periodontal bone loss, osteolytic
 XX metastasis and/or prosthetic loosening
 XX SQ Sequence 406 AA;
 Query Match 96.8%; Score 2191; DB 4; Length 406;
 Best Local Similarity 97.5%; Pred. No. 1.2e-128;
 Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;
 QY 1 ETFPKYLHYDETSHTQLLCKDCKPPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60
 DB 1 ETFPKYLHYDETSHTQLLCKDCKPPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 120
 DB 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 120
 QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSENSTQKSG--GGG 178
 DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSENSTQKSGIDVTV 180
 QY 179 GGGTCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 238
 DB 181 DKHTCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 240
 QY 239 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 298
 DB 241 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
 QY 299 GQREPOVYTLPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 358
 DB 301 GQREPOVYTLPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 360
 QY 359 DGSFFLYSKLTVDKSRWQQGNVFSVCSVMHEALHNHYTQKSLSLSPG 404
 DB 361 DGSFFLYSKLTVDKSRWQQGNVFSVCSVMHEALHNHYTQKSLSLSPG 406
 RESULT 12
 AAB66993
 ID AAB66993 standard; protein; 422 AA.
 XX AAB66993;
 XX 19-APR-2001 (first entry)
 XX OPG-Fc.
 XX Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
 KW

KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
 KW endometritis; fever; glomerulonephritis; inflammatory bowel disease;
 KW ischaemia; Parkinson's disease.
 XX Unidentified.
 XX WO200103719-A2.
 XX 18-JAN-2001.
 XX 07-JUL-2000; 2000WO-US018667.
 XX 09-JUL-1999; 99US-00350670.
 XX 09-DEC-1999; 99US-00457647.
 XX (AMGE-) AMGEN INC.
 XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
 XX WPI; 2001-103031/11.
 XX N-PSDB; AAF57869.
 XX Treating conditions leading to bone loss such as rheumatoid arthritis,
 XX multiple sclerosis and asthma, comprises administering an osteoprotegerin
 XX protein in conjunction with e.g. inhibitors of interleukin and tumor
 XX necrosis factor alpha.
 XX Disclosure; Fig 29; 316pp; English.
 XX The present invention relates to a method for treating conditions leading
 XX to bone loss. The method comprises administering a purified and isolated
 XX osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)
 XX in conjunction with other substances such as tumour necrosis factor-alpha
 XX (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
 XX modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet
 XX activating factor (PAF) antagonists. The method is useful for treating
 XX conditions leading to bone loss such as rheumatoid arthritis, multiple
 XX sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
 XX useful for treating inflammation, systemic lupus erythematosus (SLE) and
 XX graft-versus-host disease (GVHD). Other diseases that can be treated
 XX include acute pancreatitis, Alzheimer's disease, anorexia,
 XX atherosclerosis, coronary conditions (e.g. myocardial infarction),
 XX cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
 XX inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
 XX psoriasis and septic shock
 XX SQ Sequence 422 AA;
 Query Match 96.8%; Score 2191; DB 4; Length 422;
 Best Local Similarity 97.8%; Pred. No. 1.2e-128;
 Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;
 QY 1 ETFPKYLHYDETSHTQLLCKDCKPPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60
 DB 22 ETFPKYLHYDETSHTQLLCKDCKPPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 81
 QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 120
 DB 82 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 141
 QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSENSTQKSGGGG 180
 DB 142 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSENSTQKV---DK 197
 QY 181 GGTCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 240
 DB 198 THTCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 257
 QY 241 EVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
 DB 258 EVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 317

QY 301 PREPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 360
DB 318 PREPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 377
QY 361 SFFLYSLKLTVDKSRWQGNVFSVMEALHNHYTKLSLSPG 404
DB 378 SFFLYSLKLTVDKSRWQGNVFSVMEALHNHYTKLSLSPG 421

RESULT 13
ABJ37103
ID ABJ37103 standard; protein; 659 AA.
XX
AC ABJ37103;
XX
DT
XX
XX 08-MAY-2003 (first entry)
XX Concatameric immunoadhesion human protein sequence SEQ ID No 12.
XX Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW dimeric protein; inflammation; septicemia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation; human.
XX
XX Homo sapiens.
XX
XX WO2003010202-A1.
XX
XX PD 06-FEB-2003.
XX
XX PF 26-JUL-2002; 2002WO-KR001427.
XX
XX PR 26-JUL-2001; 2001KR-00045028.
XX
XX PA (MEDE-) MEDEXGEN CO LTD.
XX
XX PI Chung Y, Han J, Lee H, Choi E, Kim J;
XX WPI; 2003-229639/22.
XX DR N-PSDB; ABT32046.
XX
XX PT New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.
XX
XX PS Claim 27; Page 148-152; 21pp; English.
XX
XX CC The invention relates to a novel concatameric protein comprising two
CC soluble domains, in which an N-terminus of a soluble domain of a
CC biologically active protein is linked to a C-terminus of an identical
CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC related diseases. This sequence represents the human concatameric protein
XX of the invention
XX
SQ Sequence 659 AA;

Query Match 66.3%; Score 1501.5; DB 6; Length 659;
Best Local Similarity 64.5%; Pred. No. 2.2e-85;
Matches 291; Conservative 18; Mismatches 81; Indels 61; Gaps 5;

QY 9 HYDEETSHQLCDKCPGPGTYLKHQHTAKWKTVCAPCPDHYHDTDSWHTSDCLYCSPVCKE 68
DB 214 YYDQ--TAQMCCSKSPGQGHAKVCTKTSYTDVDCSDSTYTLQNNWPECLSCGRSS 271
QY 69 LQVQECNRTNVRVCECKEGRYLEI-----EFLKHSRCPGPGVQAGTPERTVCK 122
DB 272 DQVETQACTREQNRICTCPGPGYCALSKQEGCRLCAPLKRCPGPGVARPGTETSDVYCK 331

QY 123 RCPDGFSSNETSKAPCRKHTNCVFGLLLTOKGNATHONICSGNSESTQKSGG----- 176
DB 332 PCARGTFSTTSSTIDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPO 387
QY 177 -----GGGGGG-----TCPPCPAPELL 193
DB 388 PVSTRSQHTQPTPEPSTAPSTSFLLPMGPPSPAEGSTGDABPKSCDKHTCTCPAPELL 447
QY 194 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 253
DB 448 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 507
QY 254 YNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 313
DB 508 YNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 567
QY 314 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 373
DB 568 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 627
QY 374 RWOQGNVFSVMEALHNHYTKLSLSPG 404
DB 628 RWOQGNVFSVMEALHNHYTKLSLSPG 659

RESULT 14
ADQ79910
ID ADQ79910 standard; protein; 659 AA.
XX
AC ADQ79910;
XX
DT 09-SEP-2004 (first entry)
XX
XX Human tumour necrosis factor receptor 2, mgTNFR2-TNFR2/Ig construct.
DE Human; tumour necrosis factor receptor; TNFR1; TNFR2; CTLA4; CD2; IgG;
KW immunoglobulin; concatameric fused dimer protein; immunoadhesin;
KW Fc fragment; hinge.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN KR2004009997-A.
XX
XX PD 31-JAN-2004.
XX
XX PF 26-JUL-2002; 2002KR-00045921.
XX
XX PR 26-JUL-2002; 2002KR-00045921.
XX
XX PA (MEDE-) MEDEXGEN INC.
XX
XX PI Choi EY, Han JU, Jung YH, Kim JM, Lee HJ;
XX WPI; 2004-458871/43.
XX DR N-PSDB; ADQ79909.
XX
XX PT Concatameric immunoadhesin.
XX
XX PS Claim 27; SEQ ID NO 12; 129pp; Korean.
XX
XX CC The invention relates to a concatameric fused dimer protein and
XX glycosylation modification protein providing concatameric immunoadhesin
XX with improved efficacy and stability. The concatameric protein is
XX characteristically formed by binding C-terminal of one biologically
XX active protein with N-terminal of same or different biologically active
XX protein, e.g. tumour necrosis factor receptors (TNFR1 and TNFR2), CD2 and
XX CTLA4. Two monomer proteins which are formed by fusing the extracellular
XX region of a protein participating in the same immune reaction to an
XX immunoglobulin Fc fragment, bound together at a hinge region by
XX disulphide bond to give the concatameric fused dimer protein, wherein the
XX immunoglobulin is IgG. The present sequence represents a monomeric or

CC	dimeric IgG fusion protein (or a dimeric fusion protein containing	DR	N-PSDB; ADL06638.
CC	engineered N-glycosylation sites, designated "mg").	XX	DNA type semliki forest cerebritis virus carrier for expressing IgG1 Fc
XX		PT	chimeric protein as TNF receptor.
SQ	Sequence 659 AA;	XX	
	Query Match 66.1%; Score 1501.5; DB 8; Length 659;	PS	Disclosure; Fig 6; 20pp; Chinese.
	Best Local Similarity 64.9%; Pred. No. 2.2e-85;	XX	This invention describes a novel soluble acceptor encoding a human tumour
	Matches 291; Conservative 18; Mismatches 81; Indels 61; Gaps 5;	CC	necrosis factor (TNF), immunoglobulin G1 heavy chain constant region
QY	9 HYDEETSHQLLCKPPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDECLYCSPVCKE 68	CC	chimeric protein (hustNFR:IgG1 Fc). The invention also describes a
Db	214 YDQ--TAQMCCSKSPGQHAQVCTKTSYQVCDSCEDSTYQLNWNVPECLSCGRCS 271	CC	Semliki forest cerebritis virus expression carrier which expresses the
QY	69 LQVVKQECNTHNRVCECKEGRYLEI-----EFLKHSRCPGFGVQAGTPERTVCK 122	CC	recombinant protein in high efficiency. The IgG1 Fc chimeric protein of
Db	272 QVETOACTREQNRICTRPGWYCALSKQEGCRLCAPLRKCRPGFGVARGTETSDVCK 331	CC	the invention may be used to treat rheumatoid arthritis, pyaemia, heart
QY	123 RCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKSG----- 176	CC	failure, systemic lupus erythematosus (SLE) and other autoimmune
Db	332 PCAPGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTPTSRMAPGAVHLPQ 397	CC	diseases.
QY	177 -----GGGGG-----TCPPCPAPELL 193	XX	Sequence 450 AA;
Db	388 PVSTRSQHTOPTPEPSTAPSTFLLPMGPSPPAEGSTGDAEPKSCDKTHTCPPCPAPELL 447		Query Match 66.1%; Score 1496.5; DB 7; Length 450;
QY	194 GSPSVFLFPKPKDLMISTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTPREBQ 253		Best Local Similarity 68.9%; Pred. No. 2.9e-85;
Db	448 GSPSVFLFPKPKDLMISTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTPREBQ 507		Matches 284; Conservative 20; Mismatches 77; Indels 31; Gaps 5;
QY	254 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 313	QY	9 HYDEETSHQLLCKPPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDECLYCSPVCKE 68
Db	508 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 567	Db	45 YDQ--TAQMCCSKSPGQHAQVCTKTSYQVCDSCEDSTYQLNWNVPECLSCGRCS 102
QY	314 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKS 373	QY	69 LQVVKQECNTHNRVCECKEGRYLEI-----EFLKHSRCPGFGVQAGTPERTVCK 122
Db	568 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKS 627	Db	103 QVETOACTREQNRICTRPGWYCALSKQEGCRLCAPLRKCRPGFGVARGTETSDVCK 162
QY	374 RWQGGNVFSCVMHEALHNHYTQKSLSLSPG 404	QY	123 RCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKSG----- 174
Db	628 RWQGGNVFSCVMHEALHNHYTQKSLSLSPG 658	Db	163 PCAPGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTPTSRMAPGAVHLPQ 218
	RESULT 15	QY	175 GGGGGGGG-----TCPPCPAPELLGGSPSVFLFPKPKDLMISTPEVTCVVDV 223
ADL06639	ADL06639 standard; protein; 450 AA.	Db	219 GGGGGGGGSPVPEKSCDKTHTCPPCPAPELLGGSPSVFLFPKPKDLMISTPEVTCVVDV 278
AC	ADL06639;	QY	224 VSHEDPEVKFNWYVDGVEVHNNAKTPREBQYNSTYRVSVLTVLHQDWLNGKEYKCKVSN 283
XX		Db	279 VSHEDPEVKFNWYVDGVEVHNNAKTPREBQYNSTYRVSVLTVLHQDWLNGKEYKCKVSN 338
DT	06-MAY-2004 (first entry)	QY	284 KALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 343
DE	stNFRII:IgG1 Fc protein.	Db	339 KALPAPIEKTISKAKGQPREPOVYTLPPSRDEEMTKNQVSLTCLVKGFYPSDIAVEWESNG 398
XX		QY	344 QPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRWQGGNVFSCVMHEALHNHYT 395
XX	human; tumour necrosis factor; TNF; immunoglobulin G1; heavy chain;	Db	399 QPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRWQGGNVFSCVMHEALHNHYT 450
KW	constant region; chimeric protein; hustNFR:IgG1 Fc; rheumatoid arthritis;		
KW	pyaemia; heart failure; systemic lupus erythematosus; SLE;		
XX	autoimmune disease.		
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PN	CN1408875-A.		
XX			
XX	09-APR-2003.		
XX			
PF	29-SEP-2001; 2001CN-00136032.		
XX			
PR	29-SEP-2001; 2001CN-00136032.		
XX			
PA	(VIRO-) VIROLOGY INST CHINA ACAD PREVENTIVE MEDI.		
XX			
PI	Xu C, Zhang Z;		
XX			
DR	WPI; 2003-664079/63.		

Search completed: March 8, 2005, 14:38:19
Job time : 85.7356 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:28:42 ; Search time 22.0875 Seconds
(without alignments)
1365.399 Million cell updates/sec

Title: US-09-389-782A-7

Perfect score: 2264

Sequence: 1 EFPKYLHYDSETHQLLC.....VMHEALHNYTQKSLSPG 404

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1481	65.4	518	1	US-08-385-229-4
2	1481	65.4	518	4	US-09-579-845-1
3	1481	65.4	518	4	US-09-579-845-3
4	1477.5	65.3	486	1	US-08-243-010-1
5	1332	58.8	360	3	US-09-180-100-11
6	1332	58.8	376	3	US-09-180-100-22
7	1324.5	58.5	398	4	US-09-612-033B-14
8	1299	57.4	438	1	US-08-097-827-11
9	1299	57.4	438	1	US-08-494-574-11
10	1287.5	56.9	424	3	US-09-333-593A-8
11	1245	55.0	397	4	US-09-854-864-18
12	1242.5	54.9	283	4	US-09-854-864-9
13	1242	54.9	281	4	US-09-854-864-10
14	1236	54.6	253	4	US-09-428-082B-18
15	1236	54.6	277	4	US-09-428-082B-20
16	1233.5	54.5	269	4	US-09-428-082B-10
17	1232	54.4	250	4	US-09-428-082B-1070
18	1231.5	54.4	911	2	US-08-484-438-10
19	1228	54.2	704	4	US-09-590-656-2
20	1228	54.2	704	4	US-09-733-764-2
21	1223.5	54.0	455	4	US-09-773-877B-24
22	1223.5	54.0	664	3	US-08-957-063-16
23	1223.5	54.0	664	3	US-09-487-685-16
24	1223.5	54.0	664	3	US-08-802-805D-16
25	1223.5	54.0	664	4	US-09-388-316C-16
26	1222.5	54.0	248	4	US-09-428-082B-1058
27	1222.5	54.0	252	4	US-09-428-082B-1066

28	1222	54.0	247	4	US-09-428-082B-12	Sequence 12, Appl
29	1222	54.0	248	4	US-09-428-082B-1062	Sequence 1062, Ap
30	1221.5	54.0	664	3	US-08-957-063-18	Sequence 18, Appl
31	1221.5	54.0	664	3	US-09-487-685-18	Sequence 18, Appl
32	1221.5	54.0	664	3	US-08-802-805D-18	Sequence 18, Appl
33	1221.5	54.0	664	4	US-09-388-316C-18	Sequence 18, Appl
34	1221	53.9	447	4	US-09-968-362A-22	Sequence 22, Appl
35	1217.5	53.8	449	3	US-08-897-236-23	Sequence 23, Appl
36	1217.5	53.8	449	4	US-09-500-253B-23	Sequence 23, Appl
37	1216	53.7	784	4	US-09-313-942-30	Sequence 30, Appl
38	1215.5	53.7	423	4	US-09-832-659A-44	Sequence 44, Appl
39	1215.5	53.7	1158	4	US-09-313-942-26	Sequence 26, Appl
40	1215.5	53.7	1168	4	US-09-313-942-24	Sequence 24, Appl
41	1214	53.6	592	4	US-09-313-942-8	Sequence 8, Appl
42	1213.5	53.6	388	3	US-09-131-247-16	Sequence 16, Appl
43	1213.5	53.6	388	4	US-09-784-623-16	Sequence 16, Appl
44	1212.5	53.6	691	4	US-09-313-942-20	Sequence 20, Appl
45	1212.5	53.6	694	4	US-09-313-942-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-08-385-229-4
; Sequence 4, Application US/08385229
; Patent No. 5605690
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Cindy A.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Method of Treating TNF-Dependent
; TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,229
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,236
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0606
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 518 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-385-229-4

Query Match 65.4%; Score 1481; DB 1; Length 518;

Best Local Similarity 63.6%; Pred. No. 3.1e-116;

Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;

QY 9 HYDETSHQLLCDCPPGYLKHQHTAKWKTCVPCPDHYTDSWTSDECLYCSPVCKE 68

```
Db 74 YYDQ--TAQMCCKSCSPGQHAKEVCTKTSITVDCSDSTYTQIWNWVPECLSCGRCS 131
Qy 69 LQYVQECNTHNRVCECKEGRYLEI-----EFCLKHRSCTPPGFGVVOAGTPERNTVCK 122
Db 132 DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARGTETSDDVCK 191
Qy 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESSTQKSGG----- 177
Db 192 PCAPGTFSNTTSSDI CRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHL 247
Qy 178 -----GGGG-----TCPPCPAPELLG 194
Db 248 PVSTRSHTQPTPEPSTAPSTSFLLPMGSPPAEGSTGDEPKSCDKTHTCPPCPAPELLG 307
Qy 195 GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 254
Db 308 GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 367
Qy 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 314
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 427
Qy 315 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 374
Db 428 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487
Qy 375 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 404
Db 488 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 517

RESULT 2
US-09-579-845-1
; Sequence 1, Application US/09579845
; Patent No. 6537540
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-1

Query Match 65.4%; Score 1481; DB 4; Length 518;
Best Local Similarity 63.6%; Pred. No. 3.1e-116;
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;

Qy 9 HYDEETSHQLLCKCPGTYLKQHCCTAKWKTVCAPCPDHYVYDTSWHTSDECLYCSPVCKE 68
Db 74 YYDQ--TAQMCCKSCSPGQHAKEVCTKTSITVDCSDSTYTQIWNWVPECLSCGRCS 131
Qy 69 LQYVQECNTHNRVCECKEGRYLEI-----EFCLKHRSCTPPGFGVVOAGTPERNTVCK 122
Db 132 DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARGTETSDDVCK 191
Qy 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESSTQKSGG----- 177
Db 192 PCAPGTFSNTTSSDI CRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHL 247
Qy 178 -----GGGG-----TCPPCPAPELLG 194
Db 248 PVSTRSHTQPTPEPSTAPSTSFLLPMGSPPAEGSTGDEPKSCDKTHTCPPCPAPELLG 307
Qy 195 GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 254
Db 308 GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 367
Qy 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 314
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 427
Qy 315 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 374
Db 428 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487

US-09-579-845-1
; Sequence 1, Application US/09579845
; Patent No. 6537540
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-1

Query Match 65.4%; Score 1481; DB 4; Length 518;
Best Local Similarity 63.6%; Pred. No. 3.1e-116;
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;

Qy 9 HYDEETSHQLLCKCPGTYLKQHCCTAKWKTVCAPCPDHYVYDTSWHTSDECLYCSPVCKE 68
Db 74 YYDQ--TAQMCCKSCSPGQHAKEVCTKTSITVDCSDSTYTQIWNWVPECLSCGRCS 131
Qy 69 LQYVQECNTHNRVCECKEGRYLEI-----EFCLKHRSCTPPGFGVVOAGTPERNTVCK 122
Db 132 DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARGTETSDDVCK 191
Qy 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESSTQKSGG----- 177
Db 192 PCAPGTFSNTTSSDI CRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHL 247
Qy 178 -----GGGG-----TCPPCPAPELLG 194
Db 248 PVSTRSHTQPTPEPSTAPSTSFLLPMGSPPAEGSTGDEPKSCDKTHTCPPCPAPELLG 307
```

```
Qy 195 GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 254
Db 308 GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 367
Qy 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 314
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 427
Qy 315 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 374
Db 428 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487
Qy 375 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 404
Db 488 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 517

RESULT 3
US-09-579-845-3
; Sequence 3, Application US/09579845
; Patent No. 6537540
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/09/579,845
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-3

Query Match 65.4%; Score 1481; DB 4; Length 518;
Best Local Similarity 63.6%; Pred. No. 3.1e-116;
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;

Qy 9 HYDEETSHQLLCKCPGTYLKQHCCTAKWKTVCAPCPDHYVYDTSWHTSDECLYCSPVCKE 68
Db 74 YYDQ--TAQMCCKSCSPGQHAKEVCTKTSITVDCSDSTYTQIWNWVPECLSCGRCS 131
Qy 69 LQYVQECNTHNRVCECKEGRYLEI-----EFCLKHRSCTPPGFGVVOAGTPERNTVCK 122
Db 132 DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARGTETSDDVCK 191
Qy 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESSTQKSGG----- 177
Db 192 PCAPGTFSNTTSSDI CRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHL 247
Qy 178 -----GGGG-----TCPPCPAPELLG 194
Db 248 PVSTRSHTQPTPEPSTAPSTSFLLPMGSPPAEGSTGDEPKSCDKTHTCPPCPAPELLG 307
Qy 195 GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 254
Db 308 GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 367
Qy 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 314
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 427
Qy 315 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 374
Db 428 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487
```

```
QY 375 WOQGNVFCSCVMHEALHNHYTKLSLSPG 404
Db 488 WOQGNVFCSCVMHEALHNHYTKLSLSPG 517

RESULT 4
US-08-243-010-1
; Sequence 1, Application US/08243010
; Patent No. 5639597
; GENERAL INFORMATION:
; APPLICANT: Lauffer, Leander
; APPLICANT: Zettlmeisel, Gerd
; APPLICANT: Oquendo, Patricia
; TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
; TITLE OF INVENTION: Production and Use Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,010
; FILING DATE: 13-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/798,564
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: DE P 40 37 837.3
; FILING DATE: 28-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 02481-1132-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 486 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-243-010-1

Query Match 65.3%; Score 1477.5; DB 1; Length 486;
Best Local Similarity 64.3%; Pred. No. 5.6e-116;
Matches 288; Conservative 18; Mismatches 83; Indels 59; Gaps 5;

QY 9 HYDEETSHQLCDKCPGTYLKHCTAKWTVCAPCPDHVYTDSDWHTSDECLYSPVCKE 68
Db 45 YDQ--TAQWCSKCSFGQHAQVCTYTDVDCSDCEDSTYTLQWVVECLSCGRCS 102
QY 69 LQVVKQECNRTHNRVCEKGRYLEI-----EFLCKHRSCTPPGFGVQAGTPERNTVCK 122
Db 103 DQVETQACTREQNRICTCPGWTYCALSKQGCRLCAPLKRCPGFGVARGTETS DVVCK 162
QY 123 RCPDGFNETSSKAPCRHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGG----- 176
Db 163 PCAPGTFSNTTSDICRPHQICNVVAI-----PGNASMDVACTSTSTPTSMAPGAVHLFPQ 218
QY 177 -----GGGGGCTCPCPAPELLGGP 196
Db 219 PVSTRSQHTOPTPEPTAPSTSTFLPMGSPPAEDPEEPKSCDKTHTCTCPAPELLGGP 278

QY 197 SVFLPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREQYNS 256
Db 279 SVFLPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREQYNS 338
QY 257 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 316
Db 339 TYRVVSVLTVLHQ--WLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 397
QY 317 TNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 376
Db 398 TNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 457
QY 377 QGNVFSCSVMEALHNHYTKLSLSPG 404
Db 458 QGNVFSCSVMEALHNHYTKLSLSPG 485

RESULT 5
US-09-180-100-11
; Sequence 11, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-11

Query Match 58.8%; Score 1332; DB 3; Length 360;
Best Local Similarity 66.7%; Pred. No. 6.5e-104;
Matches 270; Conservative 15; Mismatches 60; Indels 60; Gaps 11;

QY 8 LHYDEETSHQLCDKCPGTYLKHCTAKW-KTVCAPCPD-HYYTDSWHTSDECLYSPV 65
Db 7 LHHGQGFCHK-----PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCR-L 61
QY 66 CKELQYVKOE--CNRTHNRVCEKGRYLEIEFLCKHRSCTPP-----GFGVQAGTPERN 119
Db 62 CDGEGHLEVEINCTRTQNTKCKCKNPFNCNSTVC---EHCDCPKCEHGIIECTLTSTNT 118
QY 120 VCKRCPDGFNETSSKAPCRHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGG 179
Db 119 KCKE--EGSRSNPKS---CDK-----TH----- 137
QY 180 GGGTCCPCPAPELLGGPSVFLPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDG 239
Db 138 ---TCPPCPAPELLGGPSVFLPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDG 194
QY 240 VEVHNAKTKPREQYNSYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKG 299
Db 195 VEVHNAKTKPREQYNSYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKG 254
QY 300 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSD 359
Db 255 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSD 314
QY 360 GSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTKLSLSPG 404
Db 315 GSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTKLSLSPG 359

RESULT 6
US-09-180-100-22
```

; Sequence 22, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-2079
; CURRENT APPLICATION NUMBER: US/09/180,100
; EARLIER FILING DATE: 1998-11-02
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-22

Query Match 58.8%; Score 1332; DB 3; Length 376;
Best Local Similarity 66.7%; Pred. No. 6.9e-104;
Matches 270; Conservative 15; Mismatches 60; Indels 60; Gaps 11;

QY 8 LHYDETSQLLCDKCPGTYLKQHC-TAKW-KTVCAPCD-HYYTDSWHTSDECLYCSVP 65
DB 23 LHHGQFCHK---PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCR-L 77
QY 66 CKELQVVKQE--CNRTNHRVCECKEGRYLEIFCLKHRSCTP---GFGVQAGTPERNT 119
DB 78 CDHGGLVEINCTRTQNTQKCKNFFCNSTVC---EHCDCYCKEHIIECTILST 134
QY 120 VKRCPDGFSTNETSKAPCRKHTNCSVFGLLLTQKGNATHONI CSGNSESTQKSGGGG 179
DB 135 KCKE--EGSRNPEKS---CDK-----TH----- 153
QY 180 GGGTCCPCAPPELLGSPVFLPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 239
DB 154 ---TCPCCPAPPELLGSPVFLPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 210
QY 240 VEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAG 299
DB 211 VEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAG 270
QY 300 QPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD 359
DB 271 QPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD 330
QY 360 GSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
DB 331 GSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 375

RESULT 7
US-09-612-033B-14
; Sequence 14, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Saris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily
; TITLE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: Consisting of Mus musculus sequences and
; OTHER INFORMATION: Immunoglobulin sequences
US-09-612-033B-14

Query Match 58.5%; Score 1324.5; DB 4; Length 398;
Best Local Similarity 65.7%; Pred. No. 3.2e-103;
Matches 259; Conservative 24; Mismatches 62; Indels 49; Gaps 6;

QY 12 EETSHQLLCDKCPGTYLKQHC-TAKWKTVCAPCDPHYTTDSWHTSDECLYCSVPCKELQ 70
DB 52 EYMSKDVCCCKNCAGTFVKAPCEIPHTQGCCKCHPGTFTTEKNDYLDACILCS-TCDDQ 110
QY 71 YVQECNRTNHRVCECKEGRYLEIFCLKHRSCTPFGVQAGTPERNTVCKRCPDGPF 130
DB 111 EWADCSATSDRKCQCTGLY-----YDKP-----PESCRPTCKCQ----- 149
QY 131 NETSKAPCRKHTNCSVFGLLLTQKGNATHONI CSGNSESTQKSGGGGGTCCPCAP 190
DB 150 -----GIPVQECNSTANTVCSSSVSNVDTH-----TCPPCAP 183
QY 191 ELLGGSPVFLPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKR 250
DB 184 ELLGGSPVFLPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKR 243
QY 251 BEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAGQPREPOVYTL 310
DB 244 BEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAGQPREPOVYTL 303
QY 311 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV 370
DB 304 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV 363
QY 371 DKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
DB 364 DKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 397

RESULT 8
US-09-827-11
; Sequence 11, Application US/08097827
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; Goodwin, Ray
; Fanslow, William
; Gayle, Richard
; TITLE OF INVENTION: Novel Cytokine which is a Ligand for
; OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-Jul-1993
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkihs, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-097-827-11

Query Match          57.4%; Score 1299; DB 1; Length 438;
Best Local Similarity 60.4%; Pred. No. 5e-101;
Matches 258; Conservative 22; Mismatches 77; Indels 70; Gaps 6;

QY 20 CDKCPPTGTYLKQHTAKWKTVCAPCPDHYTD--SWHTSDECLYCSPVCKELQYVKQECN 77
Db 39 CRECPQGHGMVNRCDHTRDTLCHPCETGFYNEAVNYDTCKQCTQCNH--RSGSELQNCT 96
QY 78 RTHNRVCECKEGYLEIEFCLKHRSCPPGFGVVQAGTPERNVTCKRCPDGFFSNETSKA 137
Db 97 PTQDTVCRCR-----PGTQPRQDSGYKLGVDVCPGPHFS--PGNNQ 137
QY 138 PCRKHTNCSVFGLLLTQKGNATHDNICSGNS----- 168
Db 138 ACKPWTNCTLSGKQTRHPASDSLDVACEDRSLLATLLMETQRTPTTQSTVWPRTS 197
QY 169 -----ESTQKSGGGGGGTCPPCPAPELLGSPVFLFPPKPKDTLMISRTPEV 217
Db 198 ELPSTPTLVEPRSCDKT-----HTCPCPAPAEAGAPSVFLFPPKPKDTLMISRTPEV 250
QY 218 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLDHODWLNKEY 277
Db 251 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLDHODWLNKEY 310
QY 278 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 337
Db 311 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 370
QY 338 EWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSVMHAEALHNYTOK 397
Db 371 EWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSVMHAEALHNYTOK 430
QY 398 SLSLSPG 404
Db 431 SLSLSPG 437

RESULT 9
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 530
; PRIOR FILING DATE: 1997-05-09
```

```
;
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-11

Query Match          57.4%; Score 1299; DB 1; Length 438;
Best Local Similarity 60.4%; Pred. No. 5e-101;
Matches 258; Conservative 22; Mismatches 77; Indels 70; Gaps 6;

QY 20 CDKCPPTGTYLKQHTAKWKTVCAPCPDHYTD--SWHTSDECLYCSPVCKELQYVKQECN 77
Db 39 CRECPQGHGMVNRCDHTRDTLCHPCETGFYNEAVNYDTCKQCTQCNH--RSGSELQNCT 96
QY 78 RTHNRVCECKEGYLEIEFCLKHRSCPPGFGVVQAGTPERNVTCKRCPDGFFSNETSKA 137
Db 97 PTQDTVCRCR-----PGTQPRQDSGYKLGVDVCPGPHFS--PGNNQ 137
QY 138 PCRKHTNCSVFGLLLTQKGNATHDNICSGNS----- 168
Db 138 ACKPWTNCTLSGKQTRHPASDSLDVACEDRSLLATLLMETQRTPTTQSTVWPRTS 197
QY 169 -----ESTQKSGGGGGGTCPPCPAPELLGSPVFLFPPKPKDTLMISRTPEV 217
Db 198 ELPSTPTLVEPRSCDKT-----HTCPCPAPAEAGAPSVFLFPPKPKDTLMISRTPEV 250
QY 218 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLDHODWLNKEY 277
Db 251 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLDHODWLNKEY 310
QY 278 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 337
Db 311 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 370
QY 338 EWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSVMHAEALHNYTOK 397
Db 371 EWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSVMHAEALHNYTOK 430
QY 398 SLSLSPG 404
Db 431 SLSLSPG 437

RESULT 10
US-09-333-593A-8
; Sequence 8, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R. A.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
```

; PRIOR APPLICATION NUMBER: 60/041,230
 ; PRIOR FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 424
 ; TYPE: PR
 ; ORGANISM: HOMO SAPIENS
 US-09-333-593A-8

Query Match 56.9%; Score 1287.5; DB 3; Length 424;
 Best Local Similarity 67.0%; Pred. No. 4.4e-100;
 Matches 260; Conservative 15; Mismatches 62; Indels 51; Gaps 8;

QY 23 CPPTYLKHCHTAKWTVCAFCP-DHYTDSWHTSDECLYSPVCKELOYVQECNRTN 81
 DB 81 CPGHHISED-----GRDCISCKYGQDYSTQWNDLLFLCLACTR-CDSGEVLESPCTTRN 134
 QY 82 RVECKEGRYLE---IBFCLKHRS-CPGFGVVOAGTPERTNTVKCRCPDGFNSNETSKA 137
 DB 135 TVCQCEGTREEDSPMCKRCKRTGCPGMVKVGDCTPMSDIEC----- 178
 QY 138 PCRKHTNCSVFGLLLTOK-GNATHDNICSGNSESTQSGGGGGGGTCCPCPAPPELLGGP 196
 DB 179 -VHKESRSIEGRGTEPKSADKH-----TCPPCPAPPELLGGP 215
 QY 197 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNS 256
 DB 216 SVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNS 275
 QY 257 TYRVSVVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDEL 316
 DB 276 TYRVSVVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDEL 335
 QY 317 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLYSKLTVDKSRWQ 376
 DB 336 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLYSKLTVDKSRWQ 395
 QY 377 QGNVFCSCVMHEALHNHYTKSLSLSPG 404
 DB 396 QGNVFCSCVMHEALHNHYTKSLSLSPG 423

RESULT 11
 US-09-854-864-18
 ; Sequence 18, Application US/09854864
 ; Patent No. 6774106
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/ G70, BCMA,
 ; FILE OF INVENTION: BLYS/AGP-3, AND TACI
 ; CURRENT APPLICATION NUMBER: US/09/854,864
 ; PRIOR FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 397
 ; TYPE: PR
 ; ORGANISM: Homo sapiens
 US-09-854-864-18

Query Match 55.0%; Score 1245; DB 4; Length 397;
 Best Local Similarity 62.5%; Pred. No. 1.5e-96;
 Matches 252; Conservative 17; Mismatches 52; Indels 82; Gaps 9;

QY 44 CPDHYTDSWHTSDECLYSPVCKELOYVQECNRTNVRVCECKEGRYLEIEFCLKHRS 103

; PRIOR APPLICATION NUMBER: 60/041,230
 ; PRIOR FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 424
 ; TYPE: PR
 ; ORGANISM: HOMO SAPIENS
 US-09-333-593A-8

Query Match 54.9%; Score 1242.5; DB 4; Length 283;
 Best Local Similarity 75.0%; Pred. No. 1.6e-96;
 Matches 243; Conservative 11; Mismatches 21; Indels 49; Gaps 7;

QY 85 ECKEGRYLEIEFCLKHRSQPPGFGVVOAGTPERTNTVK-RCPDGFFSNETSAP---CR 140
 DB 4 QCSQNEYFD---SLH-ACIP-----CQLRC-----SSNTPPLTQC 35
 QY 141 KHTNCSVFGLLLTOKGNATHDNICSGNSESTQSGGGGGGGTCCPCPAPPELLGGPSVFL 200
 DB 36 RYCNASV-----TNSVKGNTAGGGGDKTHTCCPCPAPPELLGGPSVFL 78
 QY 201 FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNSYRV 260
 DB 79 FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNSYRV 138
 QY 261 VSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDELTKNQ 320
 DB 139 VSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDELTKNQ 198
 QY 321 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGNV 380

; PRIOR APPLICATION NUMBER: 60/041,230
 ; PRIOR FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 424
 ; TYPE: PR
 ; ORGANISM: HOMO SAPIENS
 US-09-333-593A-8

Query Match 54.9%; Score 1242.5; DB 4; Length 283;
 Best Local Similarity 75.0%; Pred. No. 1.6e-96;
 Matches 243; Conservative 11; Mismatches 21; Indels 49; Gaps 7;

QY 85 ECKEGRYLEIEFCLKHRSQPPGFGVVOAGTPERTNTVK-RCPDGFFSNETSAP---CR 140
 DB 4 QCSQNEYFD---SLH-ACIP-----CQLRC-----SSNTPPLTQC 35
 QY 141 KHTNCSVFGLLLTOKGNATHDNICSGNSESTQSGGGGGGGTCCPCPAPPELLGGPSVFL 200
 DB 36 RYCNASV-----TNSVKGNTAGGGGDKTHTCCPCPAPPELLGGPSVFL 78
 QY 201 FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNSYRV 260
 DB 79 FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNSYRV 138
 QY 261 VSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDELTKNQ 320
 DB 139 VSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDELTKNQ 198
 QY 321 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGNV 380

```
Db 199 VSLTCLVKGFPSPDIAVEWESNGQPNYYKTTTPVLDSDGSPFLYSLKLTVDKSRWQGNV 258
Qy 381 FSCVMHEALHNYTKQSLSPG 404
Db 259 FSCVMHEALHNYTKQSLSPG 282
RESULT 13
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10
Query Match 54.9%; Score 1242; DB 4; Length 281;
Best Local Similarity 84.7%; Pred. No. 1.7e-96;
Matches 238; Conservative 5; Mismatches 24; Indels 14; Gaps 3;
Qy 128 PFSNETSSKAPCRKHTNCVFGLLLTQKGNATHDNCSESTQKSGGGGGG---T 183
Db 10 YFDSLHACKPC--HLRCS-----NPPATCQPYCDPSVTSVSGSYTGGGGGDKTHT 59
Qy 184 CPPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWTVDGVVH 243
Db 60 CPPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWTVDGVVH 119
Qy 244 NAKTKPREQYNSTYRVSVLTVLHQDLNGLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 303
Db 120 NAKTKPREQYNSTYRVSVLTVLHQDLNGLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 179
Qy 304 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPF 363
Db 180 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPF 239
Qy 364 LYSKLTVDKSRWQGNVFSVCSVMHEALHNYTKQSLSPG 404
Db 240 LYSKLTVDKSRWQGNVFSVCSVMHEALHNYTKQSLSPG 280
RESULT 14
US-09-428-082B-18
; Sequence 18, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; CURRENT APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-Fc
US-09-428-082B-18
Query Match 54.6%; Score 1236; DB 4; Length 253;
Best Local Similarity 97.5%; Pred. No. 4.8e-96;
Matches 230; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
Qy 173 KSGGGGGGG---TCPPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHED 228
Db 41 KPQGGGGGGDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHED 100
Qy 229 PEVKFNWTVDGVVFNNAKTKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYKCKVSNKALPA 288
Db 101 PEVKFNWTVDGVVFNNAKTKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYKCKVSNKALPA 160
Qy 289 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 348
Db 161 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 220
Qy 349 YKTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKQSLSPG 404
Db 221 YKTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKQSLSPG 276
```

```
; SEQ ID NO 18
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-Fc
US-09-428-082B-18
Query Match 54.6%; Score 1236; DB 4; Length 253;
Best Local Similarity 97.5%; Pred. No. 4.8e-96;
Matches 230; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
Qy 173 KSGGGGGGG---TCPPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHED 228
Db 17 KPQGGGGGGDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHED 76
Qy 229 PEVKFNWTVDGVVFNNAKTKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYKCKVSNKALPA 288
Db 77 PEVKFNWTVDGVVFNNAKTKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYKCKVSNKALPA 136
Qy 289 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 348
Db 137 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 196
Qy 349 YKTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKQSLSPG 404
Db 197 YKTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKQSLSPG 252
```

```
RESULT 15
US-09-428-082B-20
; Sequence 20, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-EMP-Fc
US-09-428-082B-20
Query Match 54.6%; Score 1236; DB 4; Length 277;
Best Local Similarity 97.5%; Pred. No. 5.4e-96;
Matches 230; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
Qy 173 KSGGGGGGG---TCPPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHED 228
Db 41 KPQGGGGGGDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHED 100
Qy 229 PEVKFNWTVDGVVFNNAKTKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYKCKVSNKALPA 288
Db 101 PEVKFNWTVDGVVFNNAKTKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYKCKVSNKALPA 160
Qy 289 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 348
Db 161 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 220
Qy 349 YKTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKQSLSPG 404
Db 221 YKTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKQSLSPG 276
```


Search completed: March 8, 2005, 14:48:14
Job time : 23.0875 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:44:50 ; Search time 61.0417 Seconds
(without alignments)
2177.757 Million cell updates/sec

Title: US-09-389-782A-7
Perfect score: 2264
Sequence: 1 ETFFPKYLHYDETSQLLC.....VMHEALNNHYTKSLSPG 404

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2264	100.0	404	10	US-09-389-782-7
2	2199	97.1	425	16	US-10-467-243-20
3	2192.5	96.8	413	10	US-09-389-782-4
4	2191.5	96.8	407	10	US-09-389-782-3
5	2191	96.8	400	10	US-09-389-782-5
6	2191	96.8	406	10	US-09-389-782-6
7	1501.5	66.3	659	14	US-10-363-427-12
8	1496	66.1	467	17	US-10-901-735-4
9	1493.5	66.0	430	14	US-10-363-427-4
10	1493.5	66.0	720	14	US-10-363-427-8
11	1481	65.4	518	14	US-10-313-852-1
12	1481	65.4	518	14	US-10-313-852-3
13	1481	65.4	518	14	US-10-314-033-1
Sequence 7, Appli					
Sequence 20, Appli					
Sequence 4, Appli					
Sequence 3, Appli					
Sequence 5, Appli					
Sequence 6, Appli					
Sequence 12, Appli					
Sequence 4, Appli					
Sequence 8, Appli					
Sequence 1, Appli					
Sequence 3, Appli					
Sequence 1, Appli					

14	1481	65.4	518	14	US-10-314-033-3	Sequence 3, Appli
15	1481	65.4	518	15	US-10-423-507-1	Sequence 1, Appli
16	1436.5	63.4	444	16	US-10-467-243-24	Sequence 24, Appli
17	1435.5	63.4	443	14	US-10-151-071-5	Sequence 5, Appli
18	1435.5	63.4	443	14	US-10-166-232A-5	Sequence 5, Appli
19	1361.5	60.1	608	14	US-10-363-427-10	Sequence 10, Appli
20	1351.5	59.8	444	14	US-10-363-427-2	Sequence 2, Appli
21	1353.5	59.8	628	14	US-10-363-427-6	Sequence 6, Appli
22	1332	58.8	360	9	US-09-949-713-11	Sequence 11, Appli
23	1332	58.8	376	9	US-09-949-713-22	Sequence 22, Appli
24	1332	58.8	376	14	US-10-084-139-10	Sequence 10, Appli
25	1325.5	58.5	396	14	US-10-193-616-14	Sequence 14, Appli
26	1324.5	58.5	398	15	US-10-622-407-14	Sequence 14, Appli
27	1257.5	55.5	347	15	US-10-272-899A-108	Sequence 108, Appli
28	1252.5	55.3	380	9	US-09-948-018-39	Sequence 39, Appli
29	1246	55.0	404	9	US-09-948-018-16	Sequence 16, Appli
30	1245	55.0	397	9	US-09-854-864-18	Sequence 18, Appli
31	1245	55.0	397	9	US-09-855-158-18	Sequence 18, Appli
32	1243	54.9	446	9	US-09-792-200B-10	Sequence 10, Appli
33	1242.5	54.9	283	9	US-09-854-864-9	Sequence 9, Appli
34	1242.5	54.9	283	9	US-09-855-158-9	Sequence 9, Appli
35	1242	54.9	281	9	US-09-854-864-10	Sequence 10, Appli
36	1242	54.9	281	9	US-09-855-158-10	Sequence 10, Appli
37	1240	54.8	462	15	US-10-385-802-32	Sequence 32, Appli
38	1240	54.8	489	15	US-10-385-802-30	Sequence 30, Appli
39	1240	54.8	588	15	US-10-385-802-28	Sequence 28, Appli
40	1240	54.8	648	15	US-10-385-802-24	Sequence 24, Appli
41	1240	54.8	665	15	US-10-385-802-26	Sequence 26, Appli
42	1240	54.8	697	15	US-10-385-802-48	Sequence 48, Appli
43	1240	54.8	705	15	US-10-385-802-22	Sequence 22, Appli
44	1240	54.8	726	15	US-10-385-802-20	Sequence 20, Appli
45	1240	54.8	883	15	US-10-385-802-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-389-782-7
; Sequence 7, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389, 782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-7

Query Match 100.0%; Score 2264; DB 10; Length 404;
Best Local Similarity 100.0%; Pred. No. 9, 7e-137;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ETFFPKYLHYDETSQLLC	CDKCPGTYLKQHKTA	KWTVCA	PCPDHYTDS	WHTSDECL	60
DB	1	ETFFPKYLHYDETSQLLC	CDKCPGTYLKQHKTA	KWTVCA	PCPDHYTDS	WHTSDECL	60
QY	61	YCSVPCKEIQYVKOE	NRTHNRVCECKEGR	YLEIFELCKHRS	CPPGVVG	YVAGT	PERNTV 120
DB	61	YCSVPCKEIQYVKOE	NRTHNRVCECKEGR	YLEIFELCKHRS	CPPGVVG	YVAGT	PERNTV 120
QY	121	CKRCPDGFPSNETSS	KAPCKHTNC	SVFGLLLTKGNATHD	NICSGNSE	STQSGGGGG	180
DB	121	CKRCPDGFPSNETSS	KAPCKHTNC	SVFGLLLTKGNATHD	NICSGNSE	STQSGGGGG	180

QY 181 GGTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 240
DB 181 GGTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 240
QY 241 EVHNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISAKGQ 300
DB 241 EVHNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISAKGQ 300
QY 301 PREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPVLDSDG 360
DB 301 PREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPVLDSDG 360
QY 361 SFELYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSLSPG 404
DB 361 SFELYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSLSPG 404

RESULT 2

US-10-467-243-20
; Sequence 20, Application US/10467243
; Publication No. US20040132971A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Holdings Ltd.
; APPLICANT: Haaning, Jesper Mortensen
; APPLICANT: Haalier, Torben
; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES
; FILE REFERENCE: 0226wo310
; CURRENT APPLICATION NUMBER: US/10/467,243
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: DK PA 2001 00214
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/267,843
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00498
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/278,320
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPG-Fc polypeptide encoded by SEQ ID NO:19
US-10-467-243-20

Query Match 97.1%; Score 2199; DB 16; Length 425;
Best Local Similarity 97.8%; Pred. No. 1.4e-132;
Matches 395; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ETPFPKYLHYDEETSHQLLCKDCPPGYLKHCTAKWTKVCAPCPDHYHYTDSWHTSDECL 60
DB 22 ETPFPKYLHYDEETSHQLLCKDCPPGYLKHCTAKWTKVCAPCPDHYHYTDSWHTSDECL 81
QY 61 YCSPVKELQYVKQECNTHNRVCECKEGRYLEIFCLKHSRCPGFGVQAGTPERNTV 120
DB 82 YCSPVKELQYVKQECNTHNRVCECKEGRYLEIFCLKHSRCPGFGVQAGTPERNTV 141
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNI CSGNSESTOKSGGGGG 180
DB 142 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNI CSGNSESTOKLEKSDK 201
QY 181 GGTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 240
DB 202 THTCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 261
QY 241 EVHNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISAKGQ 300
DB 262 EVHNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISAKGQ 321
QY 301 PREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPVLDSDG 360

DB 322 PREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPVLDSDG 381
QY 361 SFELYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSLSPG 404
DB 382 SFELYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSLSPG 425

RESULT 3

US-09-389-782-4
; Sequence 4, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-4

Query Match 96.8%; Score 2192.5; DB 10; Length 413;
Best Local Similarity 95.9%; Pred. No. 3.7e-132;
Matches 396; Conservative 0; Mismatches 8; Indels 9; Gaps 1;
QY 1 ETPFPKYLHYDEETSHQLLCKDCPPGYLKHCTAKWTKVCAPCPDHYHYTDSWHTSDECL 60
DB 1 ETPFPKYLHYDEETSHQLLCKDCPPGYLKHCTAKWTKVCAPCPDHYHYTDSWHTSDECL 60
QY 61 YCSPVKELQYVKQECNTHNRVCECKEGRYLEIFCLKHSRCPGFGVQAGTPERNTV 120
DB 61 YCSPVKELQYVKQECNTHNRVCECKEGRYLEIFCLKHSRCPGFGVQAGTPERNTV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNI CSGNSESTOKSGGGGG 180
DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNI CSGNSESTOKCQIDVTA 180
QY 181 GG-----TCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEV 231
DB 181 AAEPKSCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEV 240
QY 232 KFNWYVDGVEVHNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIE 291
DB 241 KFNWYVDGVEVHNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIE 300
QY 292 KTISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVESNGQPENNYKT 351
DB 301 KTISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVESNGQPENNYKT 360
QY 352 TPPVLDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSLSPG 404
DB 361 TPPVLDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSLSPG 413

RESULT 4

US-09-389-782-3
; Sequence 3, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-3

Query Match      96.8%; Score 2191.5; DB 10; Length 407;
Best Local Similarity 97.1%; Pred. No. 4.4e-132;
Matches 395; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 1 ETFPKYLHYDETSHTQLLCKCPGTYLKQHCTAKWKTVCAPCPHYTDSWHTSDECL 60
DB 1 ETFPKYLHYDETSHTQLLCKCPGTYLKQHCTAKWKTVCAPCPHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTPERNIV 120
DB 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTPERNIV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSESSTQKVG 177
DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSESSTQKVG 177
QY 178 GGGGTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYV 237
DB 181 CDKTHTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYV 240
QY 238 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 297
DB 241 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 300
QY 298 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTPVLD 357
DB 301 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTPVLD 360
QY 358 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 404
DB 361 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 407

RESULT 5
US-09-389-782-5
; Sequence 5, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-5

Query Match      96.8%; Score 2191; DB 10; Length 400;
Best Local Similarity 97.8%; Pred. No. 4.4e-132;
Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

QY 1 ETFPKYLHYDETSHTQLLCKCPGTYLKQHCTAKWKTVCAPCPHYTDSWHTSDECL 60
DB 1 ETFPKYLHYDETSHTQLLCKCPGTYLKQHCTAKWKTVCAPCPHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTPERNIV 120
DB 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTPERNIV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSESSTQKVG 178
DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSESSTQKVG 180
QY 179 GGGGTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYV 238
DB 181 DXHTTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYV 240
QY 239 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 298
DB 241 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 300
QY 299 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTPVLD 358
DB 301 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTPVLD 360
QY 359 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 404
DB 361 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 406

RESULT 6
US-09-389-782-6
; Sequence 6, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-6

Query Match      96.8%; Score 2191; DB 10; Length 406;
Best Local Similarity 97.5%; Pred. No. 4.5e-132;
Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 1 ETFPKYLHYDETSHTQLLCKCPGTYLKQHCTAKWKTVCAPCPHYTDSWHTSDECL 60
DB 1 ETFPKYLHYDETSHTQLLCKCPGTYLKQHCTAKWKTVCAPCPHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTPERNIV 120
DB 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTPERNIV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSESSTQKVG 178
DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNCSNSESSTQKVG 180
QY 179 GGGGTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYV 238
DB 181 DXHTTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYV 240
QY 239 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 298
DB 241 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 300
QY 299 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTPVLD 358
DB 301 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTPVLD 360
QY 359 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 404
DB 361 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 406
```

```

; CURRENT APPLICATION NUMBER: US/10/901,735
; CURRENT FILING DATE: 2004-07-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent version 3.2
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide
US-10-901-735-4

Query Match 66.1%; Score 1496; DB 17; Length 467;
Best Local Similarity 64.2%; Pred. No. 1.3e-87;
Matches 289; Conservative 20; Mismatches 81; Indels 60; Gaps 58
QY 9 HYDEETSHQLLCKCPGTYLKQHCCTAKWTKVACPCDPHYTDSWHTSDECLYCSPVCKE 68
DB 23 YYDQ--TAQMCCSKCPGQHAQVCTKTSITVCDSCEDSTYTQLNWVPECLSCGSRCS 80
QY 69 LQYVKQECNRTHNRVCEKGRYLEI-----EFLKHRSCPRGFGVQAGTPERTVCK 122
DB 81 DQVETQACTREQNRICTRCPGWYCALSKQEGCRLCAPLRCRFGFVARPGTETSDVCK 140
QY 123 RCPDGFESNETSKAPCRKHTNCVSFGLLLTQKGNATHDNICSGNSESTQKSGG---- 177
DB 141 PCAPGTFTNTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTSTSRMAPGAVHLPQ 196
QY 178 -----GGGGG-----TCPPCPAPELLG 194
DB 197 PVSTRSQHTQTPPESTAPSTSFLLPMGPSPPAEGSTGDEPKSCDKTHTCPCPAPELLG 256
QY 195 GPSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREEQ 254
DB 257 GPSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREEQ 316
QY 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 314
DB 317 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 376
QY 315 ELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 374
DB 377 EMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 436
QY 375 WQOQNVFSCSMHEALHNHYTQKSLSLSPG 404
DB 437 WQOQNVFSCSMHEALHNHYTQKSLSLSPG 466

RESULT 9
US-10-363-427-4
; Sequence 4, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: MedGen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatametric Immunoadhesion
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 4
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-427-4

; CURRENT APPLICATION NUMBER: US/10/901,735
; CURRENT FILING DATE: 2004-07-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent version 3.2
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide
US-10-901-735-4

Query Match 66.1%; Score 1496; DB 17; Length 467;
Best Local Similarity 64.2%; Pred. No. 1.3e-87;
Matches 289; Conservative 20; Mismatches 81; Indels 60; Gaps 58
QY 9 HYDEETSHQLLCKCPGTYLKQHCCTAKWTKVACPCDPHYTDSWHTSDECLYCSPVCKE 68
DB 23 YYDQ--TAQMCCSKCPGQHAQVCTKTSITVCDSCEDSTYTQLNWVPECLSCGSRCS 80
QY 69 LQYVKQECNRTHNRVCEKGRYLEI-----EFLKHRSCPRGFGVQAGTPERTVCK 122
DB 81 DQVETQACTREQNRICTRCPGWYCALSKQEGCRLCAPLRCRFGFVARPGTETSDVCK 140
QY 123 RCPDGFESNETSKAPCRKHTNCVSFGLLLTQKGNATHDNICSGNSESTQKSGG---- 177
DB 141 PCAPGTFTNTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTSTSRMAPGAVHLPQ 196
QY 178 -----GGGGG-----TCPPCPAPELLG 194
DB 197 PVSTRSQHTQTPPESTAPSTSFLLPMGPSPPAEGSTGDEPKSCDKTHTCPCPAPELLG 256
QY 195 GPSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREEQ 254
DB 257 GPSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREEQ 316
QY 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 314
DB 317 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 376
QY 315 ELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 374
DB 377 EMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 436
QY 375 WQOQNVFSCSMHEALHNHYTQKSLSLSPG 404
DB 437 WQOQNVFSCSMHEALHNHYTQKSLSLSPG 466

RESULT 9
US-10-363-427-4
; Sequence 4, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: MedGen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatametric Immunoadhesion
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 4
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-427-4

; CURRENT APPLICATION NUMBER: US/10/901,735
; CURRENT FILING DATE: 2004-07-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent version 3.2
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide
US-10-901-735-4

Query Match 66.1%; Score 1496; DB 17; Length 467;
Best Local Similarity 64.2%; Pred. No. 1.3e-87;
Matches 289; Conservative 20; Mismatches 81; Indels 60; Gaps 58
QY 9 HYDEETSHQLLCKCPGTYLKQHCCTAKWTKVACPCDPHYTDSWHTSDECLYCSPVCKE 68
DB 23 YYDQ--TAQMCCSKCPGQHAQVCTKTSITVCDSCEDSTYTQLNWVPECLSCGSRCS 80
QY 69 LQYVKQECNRTHNRVCEKGRYLEI-----EFLKHRSCPRGFGVQAGTPERTVCK 122
DB 81 DQVETQACTREQNRICTRCPGWYCALSKQEGCRLCAPLRCRFGFVARPGTETSDVCK 140
QY 123 RCPDGFESNETSKAPCRKHTNCVSFGLLLTQKGNATHDNICSGNSESTQKSGG---- 177
DB 141 PCAPGTFTNTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTSTSRMAPGAVHLPQ 196
QY 178 -----GGGGG-----TCPPCPAPELLG 194
DB 197 PVSTRSQHTQTPPESTAPSTSFLLPMGPSPPAEGSTGDEPKSCDKTHTCPCPAPELLG 256
QY 195 GPSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREEQ 254
DB 257 GPSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREEQ 316
QY 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 314
DB 317 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 376
QY 315 ELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 374
DB 377 EMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 436
QY 375 WQOQNVFSCSMHEALHNHYTQKSLSLSPG 404
DB 437 WQOQNVFSCSMHEALHNHYTQKSLSLSPG 466

RESULT 9
US-10-363-427-4
; Sequence 4, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: MedGen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatametric Immunoadhesion
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 4
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-427-4

; CURRENT APPLICATION NUMBER: US/10/901,735
; CURRENT FILING DATE: 2004-07-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent version 3.2
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide
US-10-901-735-4

Query Match 66.1%; Score 1496; DB 17; Length 467;
Best Local Similarity 64.2%; Pred. No. 1.3e-87;
Matches 289; Conservative 20; Mismatches 81; Indels 60; Gaps 58
QY 9 HYDEETSHQLLCKCPGTYLKQHCCTAKWTKVACPCDPHYTDSWHTSDECLYCSPVCKE 68
DB 23 YYDQ--TAQMCCSKCPGQHAQVCTKTSITVCDSCEDSTYTQLNWVPECLSCGSRCS 80
QY 69 LQYVKQECNRTHNRVCEKGRYLEI-----EFLKHRSCPRGFGVQAGTPERTVCK 122
DB 81 DQVETQACTREQNRICTRCPGWYCALSKQEGCRLCAPLRCRFGFVARPGTETSDVCK 140
QY 123 RCPDGFESNETSKAPCRKHTNCVSFGLLLTQKGNATHDNICSGNSESTQKSGG---- 177
DB 141 PCAPGTFTNTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTSTSRMAPGAVHLPQ 196
QY 178 -----GGGGG-----TCPPCPAPELLG 194
DB 197 PVSTRSQHTQTPPESTAPSTSFLLPMGPSPPAEGSTGDEPKSCDKTHTCPCPAPELLG 256
QY 195 GPSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREEQ 254
DB 257 GPSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREEQ 316
QY 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 314
DB 317 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 376
QY 315 ELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 374
DB 377 EMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 436
QY 375 WQOQNVFSCSMHEALHNHYTQKSLSLSPG 404
DB 437 WQOQNVFSCSM
```

```

Query Match      66.0%; Score 1493.5; DB 14; Length 490;
Best Local Similarity 64.3%; Pred. No. 1.9e-87;
Matches 290; Conservative 18; Mismatches 82; Indels 61; Gaps 5;

QY 9 HYDEETSHQLLCKDCKPPGTYLKQHCTAKWKTVCAPCPDPHYTDSMHTSDECLYCSVPVCKE 68
DB 45 YYDQ--TAQMCCSKCSPQHAKVFTKTSVDVCDSCEDSTYTQLWNWVPECLSCGSRCSS 102
QY 69 LQYVKQECNRTHNRVCECKEGRYLEI-----EFLCHKRSPPGFGVVQAGTPERNVTCK 122
DB 103 DQVETOACTREONRICTCRPGWCALSKQEGCRLCAPLRCRPGFVARPGTETSDVVCK 162
QY 123 RCPDGFPSNETSSKAPCRKHNTCSVFGLLLTQKNATHDNTCSGNBSSTQKSGG-----176
DB 163 PCAPGTFTNTTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLQP 218
QY 177 -----GGGGGG-----TCPPCPAPPELL 193
DB 219 PVSTRSQTHTPPESTAPSTSFLLPMGPPSPAEGSTGDABPKSCDKTHTCPPCPAPPELL 278
QY 194 GGSVFLEPPPKPOTLMLSRTPETVTVVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQ 253
DB 279 GGSVFLEPPPKPOTLMLSRTPETVTVVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQ 338
QY 254 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 313
DB 339 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 398
QY 314 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKKS 373
DB 399 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKKS 458
QY 374 RWQOGNVFSCSVMHEALHNHYTQKSLSLSPG 404
DB 459 RWQOGNVFSCSVMHEALHNHYTQKSLSLSPG 489

RESULT 10
US-10-363-427-8
; Sequence 8, Application US/10363427
; Publication No. US2003019538A1
; GENERAL INFORMATION:
; APPLICANT: MedExGen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatametric Immunoadhesion
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 8
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-427-8

Query Match      66.0%; Score 1493.5; DB 14; Length 720;
Best Local Similarity 64.3%; Pred. No. 2.9e-87;
Matches 290; Conservative 18; Mismatches 82; Indels 61; Gaps 5;

QY 9 HYDEETSHQLLCKDCKPPGTYLKQHCTAKWKTVCAPCPDPHYTDSMHTSDECLYCSVPVCKE 68
DB 275 YYDQ--TAQMCCSKCSPQHAKVFTKTSVDVCDSCEDSTYTQLWNWVPECLSCGSRCSS 332
QY 69 LQYVKQECNRTHNRVCECKEGRYLEI-----EFLCHKRSPPGFGVVQAGTPERNVTCK 122
DB 333 DQVETOACTREONRICTCRPGWCALSKQEGCRLCAPLRCRPGFVARPGTETSDVVCK 392

```

```
QY 255 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 314
Db 368 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 427
QY 315 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 374
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 487
QY 375 WOQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
Db 488 WOQGNVFSCSVMHEALHNHYTQKSLSLSPG 517

RESULT 12
US-10-313-852-3
; Sequence 3, Application US/10313852
; Publication No. US20030103942A1
; GENERAL INFORMATION:
; APPLICANT: Bursstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/313,852
; PRIOR FILING DATE: 2002-12-06
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-313-852-3

Query Match 65.4%; Score 1481; DB 14; Length 518;
Best Local Similarity 63.6%; Pred. No. 1.3e-86;
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;

QY 9 HYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECLYCSPVCKE 68
Db 74 YDQ--TAQMCCSKCPGQHAQVCTKTSDTVDSCDSTYTLQMNWVPECLSCGSRCS 131
QY 69 LQYVKQECNRTHNRVCECKEGRYLEI-----EFLKHSRCPGPGVQAGTPERTVCK 122
Db 132 DQVETQACTREQNRICTRPGWYCALSKQEGRLCAPLRCRPGFVARPGTETSDVCK 191
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQGNATHDNI CSGNSESTQKSGG-- 177
Db 192 PCAPGTFSTNTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHL 247
QY 178 -----GGGG-----TCPPCPAPPELLG 194
Db 248 PVSTRSQHTQTPPESTAPSTFLLPMGSPSPAEGSTGDEPKSCDKTHTCCPPAPPELLG 307
QY 195 GPSVFLPPPKDITLMISRTPEVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 254
Db 308 GPSVFLPPPKDITLMISRTPEVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 367
QY 255 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 314
Db 368 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 427
QY 315 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 374
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 487
QY 375 WOQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
Db 488 WOQGNVFSCSVMHEALHNHYTQKSLSLSPG 517

US-10-314-033-3
; Sequence 3, Application US/10314033
; Publication No. US20030113295A1
; GENERAL INFORMATION:
; APPLICANT: Bursstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
```

```
Db 488 WOQGNVFSCSVMHEALHNHYTQKSLSLSPG 517

RESULT 13
US-10-314-033-1
; Sequence 1, Application US/10314033
; Publication No. US20030113295A1
; GENERAL INFORMATION:
; APPLICANT: Bursstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/314,033
; PRIOR FILING DATE: 2002-12-06
; PRIOR FILING DATE: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-033-1

Query Match 65.4%; Score 1481; DB 14; Length 518;
Best Local Similarity 63.6%; Pred. No. 1.3e-86;
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;

QY 9 HYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECLYCSPVCKE 68
Db 74 YDQ--TAQMCCSKCPGQHAQVCTKTSDTVDSCDSTYTLQMNWVPECLSCGSRCS 131
QY 69 LQYVKQECNRTHNRVCECKEGRYLEI-----EFLKHSRCPGPGVQAGTPERTVCK 122
Db 132 DQVETQACTREQNRICTRPGWYCALSKQEGRLCAPLRCRPGFVARPGTETSDVCK 191
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQGNATHDNI CSGNSESTQKSGG-- 177
Db 192 PCAPGTFSTNTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHL 247
QY 178 -----GGGG-----TCPPCPAPPELLG 194
Db 248 PVSTRSQHTQTPPESTAPSTFLLPMGSPSPAEGSTGDEPKSCDKTHTCCPPAPPELLG 307
QY 195 GPSVFLPPPKDITLMISRTPEVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 254
Db 308 GPSVFLPPPKDITLMISRTPEVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 367
QY 255 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 314
Db 368 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 427
QY 315 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 374
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 487
QY 375 WOQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
Db 488 WOQGNVFSCSVMHEALHNHYTQKSLSLSPG 517

US-10-314-033-3
; Sequence 3, Application US/10314033
; Publication No. US20030113295A1
; GENERAL INFORMATION:
; APPLICANT: Bursstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
```

```

; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/314,033
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-033-3

```

Query Match	55.4%	Score 1481;	DB 14;	Length 518;
Best Local Similarity	63.6%	Pred. No. 1.3e-86;		
Matches 286;	Conservative 21;	Mismatches 83;	Indels 60;	Gaps 5;
QY 9	HYDEESHQLLCKDKCPGTVLKHCHAKWTKVACAPCDHYHYTDSWHTSDCLYCSPVCKE	68		
DB 74	YDQ--TAQCCSKCSQGAHVCTKTSDTVDCSDSDSTYTQLMNVVPECLSCGSRCS	131		
QY 69	LQVVKQCNTHNRVCKEGRYLEI-----EPCLKHRSCPPGFVVVQAGTPERNVTCK	122		
DB 132	DQVETQACTREQNRCTCRPGWCALSKQEGCRLCAPLRCRPGFGVARGTETSDVUCK	191		
QY 123	RCPDGFFSNSTSKAPCRKHTNCVSFGLLLTKQGNATHDMICNSGSESTOKSGG----	177		
DB 192	PCAPGFFSNSTSDICRPHQICNVVAI-----PCNASMDVACITSTSTRSMAPCAVHL	247		
QY 178	-----GGGGG-----			
DB 248	PVSTRSOHTPTPEPSTAPSTSFLLMGPSPPAEGSTGDEPKSCDKTHTCPPCPAP	307		
QY 195	GPSVFLPPPKPOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAAKT	254		
DB 308	GPSVFLPPPKPOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAAKT	367		
QY 255	NSYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVY	314		
DB 368	NSYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPMOKTISKAKGQPREPOVY	427		
QY 315	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK	374		
DB 428	ELTKNQVSLTCLVKGFYPRHIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK	487		
QY 375	WQGNVPSCSMHEALHNNHYTKQSLSLSPG	404		
DB 488	WQGNVPSCSMHEALHNNHYTKQSLSLSPG	517		

```

RESULT 15
US-10-423-507-1
; Sequence 1, Application US/10423507
; Publication No. US20030219735A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Barrie, J.
; TITLE OF INVENTION: METABOLICALLY ACTIVATED RECOMBINANT
; VIRAL VECTORS AND METHODS FOR THEIR PREPARATION AND USES
; FILE REFERENCE: 226272004302
; CURRENT APPLICATION NUMBER: US/10/423,507
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 09/634,126
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 60/160,080
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518

```

[illegible]

Search completed: March 8, 2005, 15:16:16
Job time : 69.0417 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:20:42 ; Search time 16.4652 Seconds
(without alignments)
2360.831 Million cell updates/sec

Title: US-09-389-782a-7
Perfect score: 2264
Sequence: 1 ETPPPKYLHYDETSQLLC.....VMHEALHNHYTQKSLSLSPG 404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1204	53.2	255	4 S31866	Ig gamma-1 chain C
2	1204	53.2	330	1 GHU	Ig gamma-1 chain C
3	1198	52.9	374	2 S69339	Ig heavy chain V r
4	1162	51.3	234	2 PT0207	Ig gamma chain C r
5	1146.5	50.6	377	2 A23511	Ig gamma-3 chain C
6	1144.5	50.6	377	2 A60764	Ig gamma-3 chain C
7	1137.5	50.2	326	1 G2HU	Ig gamma-2 chain C
8	1133	50.0	327	1 G4HU	Ig gamma-4 chain C
9	1125.5	49.7	289	1 G3HUM1	Ig gamma-3 heavy C
10	909	40.2	323	1 GHRB	Ig gamma chain C r
11	902.5	39.9	328	2 I47160	Ig gamma 2b chain
12	902.5	39.9	328	2 I47159	Ig gamma 2a chain
13	900.5	39.8	277	2 I47162	Ig gamma 4 chain C
14	890.5	39.3	329	1 G2GP	Ig gamma-2 chain C
15	880.5	38.9	328	2 I47158	Ig gamma 1 chain c
16	874.5	38.6	328	2 I47161	Ig gamma 3 chain c
17	850.5	37.6	470	2 S22080	Ig heavy chain pre
18	841.5	37.2	329	1 G3MSC	Ig gamma-3 chain C
19	841	37.1	308	2 C30554	Ig heavy chain C r
20	841	37.1	472	2 S31459	Ig gamma-1 chain -
21	840	37.1	333	2 PS0018	Ig gamma-2b chain
22	835.5	36.9	398	1 G3MSM	Ig gamma-3 chain C
23	824.5	36.4	326	2 PS0017	Ig gamma-1 chain C
24	822.5	36.3	444	2 PC4436	monoclonal antibod
25	812.5	35.9	334	1 G1MS	Ig gamma-1 chain C
26	812.5	35.9	331	1 G1MSM	Ig gamma-1 chain C
27	804.5	35.5	329	2 S00847	Ig gamma-2c chain
28	804	35.5	330	1 G2MSA	Ig gamma-2a chain
29	804	35.5	399	1 G2MSGM	Ig gamma-2a chain

30	804	35.5	469	2 S37483	Ig gamma-2a chain
31	797	35.2	335	1 G2MSAB	Ig gamma-2a chain
32	794	35.1	446	2 S40295	Ig gamma-2a chain
33	780.5	34.5	322	2 PS0019	Ig gamma-2a chain
34	774	34.2	405	1 G2MSBM	Ig gamma-2b chain
35	774	34.2	474	1 G2MS11	Ig gamma-2b chain
36	760.5	33.6	327	2 S06511	Ig gamma-2 chain C
37	752	33.2	475	2 S01321	Ig gamma-2b chain
38	702	31.0	180	2 I46732	Ig gamma heavy cha
39	577.5	25.5	249	2 S69340	Ig heavy chain VHI
40	574.5	25.4	218	2 A36040	Ig heavy chain V-I
41	566	25.0	152	2 S14236	Ig gamma-1 chain C
42	402	17.8	572	2 B46529	Ig Y heavy chain (
43	361	15.9	549	2 S04845	Ig heavy chain pre
44	360.5	15.9	391	1 MHHUBT	Ig mu heavy chain
45	357.5	15.8	343	2 S25644	Ig mu chain C regi

ALIGNMENTS

RESULT 1

S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filpula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match	53.2%	Score	1204;	DB	4;	Length	255;
Best Local Similarity	100.0%	Pred. No.	2e-67;				
Matches	222;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	183	TCPPCPAPPELLGGSPVFLPPPKD	TLMSRTEVTCVVVDVSHEDPEVKFNWYVDGVEV	242			
Db	33	TCPPCPAPPELLGGSPVFLPPPKD	TLMSRTEVTCVVVDVSHEDPEVKFNWYVDGVEV	92			
QY	243	HNAKTKPREEQNSTYRYVSVLT	VLHODWLNKCKVSNKALPAPIEKTISKAKGQPR	302			
Db	93	HNAKTKPREEQNSTYRYVSVLT	VLHODWLNKCKVSNKALPAPIEKTISKAKGQPR	152			
QY	303	BPQVTLTPPSRDELTKNOVSL	TCLVKGFPYSDIAVEWESNGQPENNYKTPPPVLDSDGSF	362			
Db	153	BPQVTLTPPSRDELTKNOVSL	TCLVKGFPYSDIAVEWESNGQPENNYKTPPPVLDSDGSF	212			
QY	363	FLYSKLTVDKSRWQQGNVFC	SWMEALHNHYTQKSLSLSPG	404			
Db	213	FLYSKLTVDKSRWQQGNVFC	SWMEALHNHYTQKSLSLSPG	254			

RESULT 2

GHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA

A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113/235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponserting, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primärstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KO1
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KO1; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enamide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
A;Genes: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1, 114/1, 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 53.2%; Score 1204; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.6e-67;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 183 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 242
Db 108 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 167
QY 243 HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPR 302
Db 168 HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPR 227
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 362
Db 228 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 287
QY 363 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 404
Db 288 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 329
RESULT 3
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KHA>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
Query Match 52.9%; Score 1198; DB 2; Length 374;
Best Local Similarity 99.1%; Pred. No. 6.9e-67;
Matches 220; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 183 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 242
Db 152 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 211
QY 243 HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPR 302
Db 212 HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPR 271
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 362
Db 272 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 331

QY 363 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 404
 ||||| : : : : :
 Db 332 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 373

RESULT 4

PT0207
 Ig gamma chain C region - chimpanzee
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
 C:Accession: PT0207
 R:Erlich, P.H.; Moustafa, Z.A.; Oestberg, L.
 Mol. Immunol. 28, 319-322, 1991
 A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
 A:Reference number: PT0207; MUID:91287716; PMID:2062315
 A:Accession: PT0207
 A:Molecule type: mRNA
 A:Residues: 1-234 <EHR>
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 51.3%; Score 1162; DB 2; Length 234;
 Best Local Similarity 99.1%; Pred. No. 7e-65;
 Matches 214; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 183 TCPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
 ||||| : : : : :
 Db 19 TCPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 78
 QY 243 HNAKTKPREEQYNSTRVWSVLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDGSP 302
 ||||| : : : : :
 Db 79 HNAKTKPREEQYNSTRVWSVLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDGSP 138
 QY 303 EPOVYTLPPSRDELTKNQVSLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDGSP 362
 ||||| : : : : :
 Db 139 EPOVYTLPPSRDELTKNQVSLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDGSP 198
 QY 363 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKS 398
 ||||| : : : : :
 Db 199 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKS 234

RESULT 5

A23511
 Ig gamma-3 chain C region (allotype G3m(b)) - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
 C:Accession: A23511
 R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
 Nucleic Acids Res. 14, 1779-1789, 1986
 A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cDNA
 A:Reference number: A23511; MUID:86148507; PMID:3081877
 A:Accession: A23511
 A:Molecule type: DNA
 A:Residues: 1-377 <HUC>
 C:Cross-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056
 C:Genetics:
 A:Gene: GDB:IGHG3
 A:Cross-references: GDB:119339; OMIM:147120
 A:Map position: 14q32.33-14q32.33
 A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.6%; Score 1146.5; DB 2; Length 377;
 Best Local Similarity 66.0%; Pred. No. 1e-63;
 Matches 227; Conservative 19; Mismatches 33; Indels 65; Gaps 7;

QY 76 CNRTHRVCEKGRYLEIEF-----CLKHSRSC---PPGFGVVQAGTPERTVTC 121
 ||||| : : : : :
 Db 83 CNVNH-KPSNTKVDKRVELKPLGDTHTTCPRCPKSCDTPPP-----C 126

QY 122 KRCPDGFFSNETSSKAP-CRKHTNCSVFGLLLTQKGNATHDNCISGNSBSTQKSGGGGG 180
 ||||| : : : : :
 Db 127 PRCPPEP-KSCDTPPPCPRCPKSCDT----- 152
 QY 181 GGTCPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 240
 ||||| : : : : :
 Db 153 PPRCPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 212
 QY 241 EVHNAKTKPREEQYNSTRVWSVLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDG 300
 ||||| : : : : :
 Db 213 EVHNAKTKPREEQYNSTRVWSVLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDG 272
 QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDG 360
 ||||| : : : : :
 Db 273 PREPQVYTLPPSRDELTKNQVSLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDG 332
 QY 361 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 404
 ||||| : : : : :
 Db 333 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 376

RESULT 6

A60764
 Ig gamma-3 chain C region, form LAT - human
 C:Species: Homo sapiens (man)
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
 C:Accession: A60764
 R:Huck, S.; Lefranc, G.; Lefranc, M.P.
 Immunogenetics 30, 250-257, 1989
 A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 converted
 A:Reference number: A60764; MUID:90007613; PMID:2571587
 A:Accession: A60764
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-377 <HUC>
 A:Cross-references: UNIPROT:Q8N4Y9
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.6%; Score 1144.5; DB 2; Length 377;
 Best Local Similarity 66.0%; Pred. No. 1.4e-63;
 Matches 227; Conservative 19; Mismatches 33; Indels 65; Gaps 7;

QY 76 CNRTHRVCEKGRYLEIEF-----CLKHSRSC---PPGFGVVQAGTPERTVTC 121
 ||||| : : : : :
 Db 83 CNVNH-KPSNTKVDKRVELKPLGDTHTTCPRCPKSCDTPPP-----C 126
 QY 122 KRCPDGFFSNETSSKAP-CRKHTNCSVFGLLLTQKGNATHDNCISGNSBSTQKSGGGGG 180
 ||||| : : : : :
 Db 127 PRCPPEP-KSCDTPPPCPRCPKSCDT----- 152
 QY 181 GGTCPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 240
 ||||| : : : : :
 Db 153 PPRCPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 212
 QY 241 EVHNAKTKPREEQYNSTRVWSVLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDG 300
 ||||| : : : : :
 Db 213 EVHNAKTKPREEQYNSTRVWSVLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDG 272
 QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDG 360
 ||||| : : : : :
 Db 273 PREPQVYTLPPSRDELTKNQVSLTCLVKGFPSPDI AVEWESNGQPNKYKTPPPVLDSDG 332
 QY 361 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 404
 ||||| : : : : :
 Db 333 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 376

RESULT 7

G2HU
 Ig gamma-2 chain C region - human

C:Species: Homo sapiens (man)
 C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
 C:Accession: A93906; A92809; A90752; A93132; A02148
 R:Ellison, J.; Hood, L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
 A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant regions
 A:Reference number: A93906; MUID:82197621; PMID:6804948
 A:Accession: A93906
 A:Molecule type: DNA
 A:Residues: 1-326 <ELL>
 A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; F
 A:Note: Lys-326 is probably removed posttranslationally
 R:Wang, A.C.; Tung, E.; Eudenberg, H.H.
 J. Immunol. 125, 1048-1054, 1980
 A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
 A:Reference number: A92809; MUID:81007873; PMID:6774012
 A:Contents: myeloma protein Til
 A:Accession: A92809
 A:Molecule type: protein
 A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
 A:Note: Trp-156 is at or near the complement-binding site
 R:Connell, G.E.; Parr, D.M.; Hofmann, T.
 Can. J. Biochem. 57, 758-767, 1979
 A:Title: The amino acid sequences of the three heavy chain constant region domains of a
 A:Reference number: A90752; MUID:80001357; PMID:113060
 A:Contents: myeloma protein Zie
 A:Accession: A90752
 A:Molecule type: protein
 A:Residues: 1-24, 'E', 26-57, 'EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
 A:Note: This sequence has since been revised
 R:Hofmann, T.; Parr, D.M.
 Mol. Immunol. 16, 923-925, 1979
 A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G
 A:Reference number: A93132; MUID:80114419; PMID:118920
 A:Contents: Zie
 A:Accession: A93132
 A:Molecule type: protein
 A:Residues: 238-275 <HOF>
 R:Hofmann, T.; Parr, D.M.
 submitted to the Atlas, March 1980
 A:Reference number: A94591
 A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
 A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
 ned
 R:Milstein, C.; Frangione, B.
 Biochem. J. 121, 217-225, 1971
 A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
 A:Reference number: A90253; MUID:72033500; PMID:4940472
 A:Contents: annotation; myeloma protein Sa, disulfide bonds
 R:Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A:Title: Structural studies of immunoglobulin G.
 A:Reference number: A93157; MUID:69064124; PMID:5782707
 A:Contents: annotation; Sa, disulfide bonds
 C:Genetics:
 A:Gene: GDB:IGHG2
 A:Cross-references: GDB:119338; OMIM:147110
 A:Map position: 14q32.33-14q32.33
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:133-202/Domain: immunoglobulin homology <IM2>
 F:239-306/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83, 140-200, 246-304/Disulfide bonds: #status experimental
 F:102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 50.2%; Score 1137.5; DB 1; Length 326;
 Best Local Similarity 94.1%; Pred. No. 3.2e-63;
 Matches 208; Conservative 8; Mismatches 4; Indels 1; Gaps 1;
 181 GTCPCPCAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240
 103 GPPCSCPAPELGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 162
 241 EVHNATKPREQFNSTYRVSVLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 300
 163 EVHNATKPREQFNSTYRVSVLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 222
 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 360
 223 PREPQVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 282

QY 184 CTPCPCAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 243
 Db 106 CTPCPCAPP-VAGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 164
 QY 244 NAKTKPREQFNSTYRVSVLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 303
 Db 165 NAKTKPREQFNSTYRVSVLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 224
 QY 304 PQVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 363
 Db 225 PQVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 284
 QY 364 LYSKLTVDKSRWQQGNVSCVMHEALHNYTQKSLSPG 404
 Db 285 LYSKLTVDKSRWQQGNVSCVMHEALHNYTQKSLSPG 325

RESULT 8

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004

R:Ellison, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A:Cross-references: UNIPROT:P01861

A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant re

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30, 81-326 <PIN>

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83, 141-201, 247-305/Disulfide bonds: #status predicted

F:106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.0%; Score 1133; DB 1; Length 327;

Best Local Similarity 92.9%; Pred. No. 6.1e-63;

Matches 208; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

181 GTCPCPCAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240

103 GPPCSCPAPELGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 162

241 EVHNATKPREQFNSTYRVSVLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 300

163 EVHNATKPREQFNSTYRVSVLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 222

301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 360

223 PREPQVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDG 282

QY 361 SPFLYSKLTVDKSRWQCNVFCSCVMHEALHNHYTKQKSLSPG 404
 Db 283 SPFLYSRLTVDKSRWQCNVFCSCVMHEALHNHYTKQKSLSLG 326

RESULT 9

G3HUWI

IG gamma-3 heavy chain disease proteins - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1979 #sequence, revision 23-Oct-1981 #text_change 16-Jul-1999

C:Accession: A90442; A9219; A90198; A93915; A02149

R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.

Biochemistry 19, 4304-4308, 1980

A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-

A:Reference number: A90442; MUID:91021548; PMID:6774747

A:Contents: heavy chain disease protein wis

A:Accession: A90442

A:Molecule type: protein

A:Residues: 1-289 <PRA>

A:Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain

A:Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co

A:Note: the sequence of residues 42-76 was taken from the reference that follows

R:Michaelsen, T.E.; Frangione, B.; Franklin, E.C.

J. Biol. Chem. 252, 883-889, 1977

A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication

A:Reference number: A92219; MUID:77118561; PMID:402363

A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein w

A:Accession: A92219

A:Molecule type: protein

A:Residues: 12-97 <MIC>

A:Note: the hinge region in gamma-3 chains is about four times as long as in other gamma

idue segment (12-28)

A:Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter

R:Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.

Biochem. Biophys. Res. Commun. 71, 907-914, 1976

A:Title: The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the

A:Reference number: A90198; MUID:77021516; PMID:823945

A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues

A:Accession: A90198

A:Molecule type: protein

A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>

A:Note: this protein lacks most of the V region, all of the CH1 region, and part of the

R:Alexander, A.; Steinmetz, M.; Barrisault, D.; Frangione, B.; Franklin, E.C.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982

A:Title: Gamma heavy chain disease in man: cDNA sequence supports partial gene deletion

A:Reference number: A93915; MUID:82247835; PMID:6808505

A:Contents: heavy chain disease protein Omm

A:Accession: A93915

A:Molecule type: mRNA

A:Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157

A:Note: a carboxyl-terminal Lys is removed posttranslationally

A:Note: this sequence may represent an allelic form or another gamma chain subclass

C:Comment: The heavy chain disease protein wis is shown.

C:Genetics:

A:Gene: GDB:IGHG3

A:Cross-references: GDB:119339; OMIM:147120

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid

F:203-270/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match

Best Local Similarity 49.7%; Score 1125.5; DB 1; Length 289;

Matches 217; Conservative 19; Mismatches 23; Indels 53; Gaps 5;

QY

97 CLKHRSCLPPGFGVVVAGTPTBNTVCKRCPCDGFSSNETSSKAP-CRKHTNGSVFGLLL 152

Db

27 CPPEKSCDTPPP-----CPKCPFP-KSCDTPPCPCPEPKSCDT----- 65

QY

153 TQKGNATHDNCISGNSESTQKSGGGGGGCTCCPCAPPELLGGPSVFLPPKPKDTLMIS 212

Db 66 -----PPPCPCAPPELLGGPSVFLPPKPKDTLMIS 97
 QY 213 RTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVTLHQDWL 272
 Db 98 RTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQQFNSTFRVSVLTVTLHQNWL 157
 QY 273 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPVVTLPPSRDELTKNQVSLTCLVKLGFP 332
 Db 158 DGKEYKCKVSNKALPAPIEKTISKAKGQPREPVVTLPPSRDEMTKNQVSLTCLVKLGFP 217
 QY 333 SDIAVEWESNGQPNENYKTTTPVLDSDGFFLYSKLTVDKSRWQCNVFCSCVMHEALHN 392
 Db 218 SDIAVEWESNGQPNENYKTTTPVLDSDGFFLYSKLTVDKSRWQCNVFCSCVMHEALHN 277
 QY 393 HYTKQKSLSPG 404
 Db 278 RFTQKSLSPG 289

RESULT 10

GHRB

IG gamma chain C region - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 24-Apr-1984 #sequence, revision 15-Nov-1984 #text change 09-Jul-2004

C:Accession: A91749; A90290; A93928; A90245; A94416; A02161

R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.

Immunogenetics 18, 387-397, 1983

A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot

A:Reference number: A91749; MUID:84030930; PMID:6313520

A:Accession: A91749

A:Molecule type: mRNA

A:Residues: 1-323 <BER>

A:Cross-references: UNIPROT:P01870

A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr

R:Pratt, D.M.; Mole, L.E.

Biochem. J. 151, 337-349, 1975

A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob

A:Reference number: A90290; MUID:76135469; PMID:1243651

A:Accession: A90290

A:Molecule type: protein

A:Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>

R:Nartens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain

A:Reference number: A93928; MUID:83299817; PMID:6193512

A:Accession: A93928

A:Molecule type: mRNA

A:Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>

A:Cross-references: GB:M16426; NID:gl6511; PIDN:AAA31289.1; PID:gl65112

A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker;

R:Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin C

A:Reference number: A90245; MUID:70110015; PMID:5461106

A:Accession: A90245

A:Molecule type: protein

A:Residues: 132-143, 'E', 145-161 <FRU>

R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,

A:Reference number: A94416

A:Accession: A94416

A:Molecule type: protein

A:Residues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q', ';

A:Note: this has the e15 allotypic marker, 185-Ala

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-82/Domain: immunoglobulin homology <IM1>

F:130-199/Domain: immunoglobulin homology <IM2>

F:236-303/Domain: immunoglobulin homology <IM3>

F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match 40.2%; Score 909; DB 1; Length 323;
Best Local Similarity 72.8%; Pred. No. 3.9e-49;
Matches 163; Conservative 28; Mismatches 31; Indels 2; Gaps 1;

QY 183 TC--PPCPAPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 240
Db 99 TCSKPTCPPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 158
QY 241 EVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 300
Db 159 QVTRARPLEAQDSIRVVSTLPIHQDWLNGKEYKCKVSNKALPAPIEKTISKARGQ 218
QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 360
Db 219 PLEPKVYTMGPPEELSSRSVSLTCMINGFVPSDISVEWEKNGKAEDNYKTITPAVLDSG 278
QY 361 SFELYSKLTVDKSRWQQGNVSCVSMHEALHNNHYTKQSLSPG 404
Db 279 SYFLYKLSVPTSEWQGRDFTCSVMHEALHNNHYTKQSLSPG 322

RESULT 11
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126
A:Gene: IGC2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 39.9%; Score 902.5; DB 2; Length 328;
Best Local Similarity 59.7%; Pred. No. 1e-48;
Matches 172; Conservative 36; Mismatches 53; Indels 27; Gaps 4;

QY 125 PDGFFSNETS KAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGTC 184
Db 59 PSGLYSLSSMVTVPASSLSKSY-----TCNVNHPATTTKDKRVGTGTK 103

RESULT 12
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126
A:Gene: IGC2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
```

```
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124
A:Gene: IGC2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 39.9%; Score 902.5; DB 2; Length 328;
Best Local Similarity 59.7%; Pred. No. 1e-48;
Matches 172; Conservative 36; Mismatches 53; Indels 27; Gaps 4;

QY 125 PDGFFSNETS KAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGTC 184
Db 59 PSGLYSLSSMVTVPASSLSKSY-----TCNVNHPATTTKDKRVGTGTK 103

RESULT 13
I47162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:G433129; PIDN:AAA52220.1; PID:G433130
A:Gene: IGC4
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 900.5; DB 2; Length 277;
Best Local Similarity 60.6%; Pred. No. 1.1e-48;
Matches 172; Conservative 35; Mismatches 58; Indels 19; Gaps 4;

QY 125 PDGFFSNETS KAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGTC 184
Db 8 PSGLYSLSSMVTVPASSLSKSY-----TCNVNHPATTTKDKRVGTGTK 52

QY 185 PPCP-APELLG-GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 242
Db 53 PPCPICPACGPGPSAFIPFPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 112
QY 243 HNAAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 302
```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:56 ; Search time 74.6958 Seconds
(without alignments)
2769.633 Million cell updates/sec

Title: US-09-389-782A-7
Perfect score: 2264
Sequence: 1 EFPFKYLYHDETSQILLC.....VMHEALHNHYTQKSLSPG 404

Scoring table:
BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1204	53.2	330	1 GCL_HUMAN	P01857 homo sapien
2	1204	53.2	465	2 Q6GMX6	Q6gmx6 homo sapien
3	1204	53.2	466	2 Q6IN78	Q6in78 homo sapien
4	1204	53.2	469	2 Q7Z7P5	Q7z7p5 homo sapien
5	1204	53.2	470	2 Q6PJA4	Q6pja4 homo sapien
6	1204	53.2	470	2 Q7Z5W1	Q7z5w1 homo sapien
7	1204	53.2	472	2 Q6N089	Q6n089 homo sapien
8	1204	53.2	475	2 Q6GMW7	Q6gmw7 homo sapien
9	1204	53.2	476	2 Q6GMX1	Q6gmx1 homo sapien
10	1204	53.2	679	2 Q96PQ8	Q96pq8 homo sapien
11	1200	53.0	473	2 Q6P055	Q6p055 homo sapien
12	1200	53.0	475	2 Q6MZQ6	Q6mzq6 homo sapien
13	1200	53.0	480	2 Q6N094	Q6n094 homo sapien
14	1200	53.0	481	2 Q6N097	Q6n097 homo sapien
15	1200	53.0	482	2 Q7Z351	Q7z351 homo sapien
16	1198	52.9	348	2 Q6PYX1	Q6pyx1 homo sapien
17	1198	52.9	473	2 Q6MZV7	Q6mzv7 homo sapien
18	1198	52.9	478	2 Q6P181	Q6p181 homo sapien
19	1198	52.9	480	2 Q6PJF1	Q6pjf1 homo sapien
20	1198	52.9	544	2 Q6NPJ5	Q6npj5 homo sapien
21	1197	52.9	466	2 Q6N096	Q6n096 homo sapien
22	1193	52.7	475	2 Q6N095	Q6n095 homo sapien
23	1187	52.4	487	2 Q652L2	Q652l2 mus sp. fv/
24	1146.5	50.6	354	2 Q86T72	Q86tt2 homo sapien
25	1142.5	50.5	521	2 Q8N4Y9	Q8ny9 homo sapien
26	1141.5	50.4	518	2 Q6N030	Q6n030 homo sapien
27	1137.5	50.2	326	1 GC2_HUMAN	P01859 homo sapien
28	1137.5	50.2	417	2 Q6N093	Q6n093 homo sapien
29	1136.5	50.2	509	2 Q8N17	Q8n17 homo sapien
30	1134.5	50.1	464	2 Q6MZU6	Q6mzu6 homo sapien
31	1133	50.0	327	1 GC4_HUMAN	P01861 homo sapien

RESULT 1					ALIGNMENTS				
GCL_HUMAN					STANDARD; PRT; 330 AA.				
ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.					
AC	P01857;								Q8tc63 homo sapien
DT	21-JUL-1986 (Rel. 01, Created)								Q6p6c4 homo sapien
DT	21-JUL-1986 (Rel. 01, Last sequence update)								P01860 homo sapien
DT	25-OCT-2004 (Rel. 45, Last annotation update)								Q6mzx7 homo sapien
DE	19 gamma-1 chain C region.								Q68cn4 homo sapien
GN	Name=IGHG1;								Q00300 homo sapien
OS	Homo sapiens (Human).								P01870 oryctolagus
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								Q95m34 equus caball
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								O68p12 mus musculus
OX	NCBI_TaxID=9606;								O08712 mus musculus
RN	[1]								P01862 cavia porce
RP	SEQUENCE FROM N.A.								O08727 rattus norv
RX	MEDLINE=82274238; PubMed=6287432;								P22436 mus musculus
RA	Ellison J.W., Berson B.J., Hood L.E.;								Q7tmk1 mus musculus
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."								
RL	Nucleic Acids Res. 10:4071-4079 (1982).								
RN	[2]								
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).								
RX	MEDLINE=71064024; PubMed=5489771;								
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,								
RT	Waxdal M.J., Edelman G.M.;								
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."								
RN	[3]								
RP	SEQUENCE OF 136-329 (EU).								
RX	MEDLINE=71064025; PubMed=5530842;								
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,								
RT	Edelman G.M.;								
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."								
RN	[4]								
RP	SEQUENCE (MYELOMA PROTEIN NIE).								
RX	MEDLINE=77070269; PubMed=826475;								
RA	Ponstingl H., Hilschmann N.;								
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."								
RL	Hoppe-Sayler's Z. Physiol. Chem. 357:1571-1604 (1976).								
RN	[5]								
RP	SEQUENCE (MYELOMA PROTEIN KOL). AND DISULFIDE BONDS.								
RX	MEDLINE=83289131; PubMed=6884994;								
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;								
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."								
RL	Hoppe-Sayler's Z. Physiol. Chem. 364:713-747 (1983).								
RN	[6]								
RP	DISULFIDE BONDS.								
RX	MEDLINE=71064027; PubMed=4923144;								

RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RL Intrachain disulfide bonds.";
 RN Biochemistry 9:3188-3196(1970).
 RP [7]
 RX DISULFIDE BONDS.
 RA MEDLINE=77070267; PubMed=1002129;
 RT Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
 RT characterization of the protein, the L- and H-chains, the cyanogen
 RT bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
 CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
 CC G1M(3) marker and the G1M (non-1) markers.
 CC -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,
 CC 116, 198, 269 and 272.
 CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
 CC 268-272.
 CC -!- MISCELLANEOUS: KOL also differs in the amidation states of
 CC residues 198, 267 and 272.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A93433; GHU.
 DR PDB; 1A07; X-ray; H=1-103.
 DR PDB; 1D5B; X-ray; B/H=1-101.
 DR PDB; 1D5I; X-ray; H=1-101.
 DR PDB; 1D6V; X-ray; H=1-101.
 DR PDB; 1DN2; X-ray; A/B=120-326.
 DR PDB; 1E4K; X-ray; A/B=106-329.
 DR PDB; 1FC1; X-ray; A/B=106-329.
 DR PDB; 1FC2; X-ray; D=106-329.
 DR PDB; 1FCC; X-ray; A=121-326.
 DR PDB; 1H2H; X-ray; H/K=1-330.
 DR PDB; 1I72; X-ray; B/D=1-103.
 DR PDB; 1IIS; X-ray; A/B=107-330.
 DR PDB; 1IIX; X-ray; A/B=107-330.
 DR PDB; 1L6X; X-ray; A=120-326.
 DR PDB; 1OQX; X-ray; A=120-326.
 DR PDB; 2RCS; X-ray; H=1-103.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; --
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 DR 3D-structure; Direct protein sequencing; Glycoprotein;
 KW Immunoglobulin C region; Immunoglobulin domain.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT 99 110 Hinge.

FT DOMAIN 111 223
 FT DOMAIN 224 330
 FT DISULFID 27 83
 FT DISULFID 103 103
 FT DISULFID 109 109
 FT DISULFID 112 112
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT VARIANT 97 97
 FT N-linked (GlcNAc. . .).
 FT K -> R (in G1M(3) marker).
 FT /FTid=VAR_003886.
 FT D -> E (in G1M(non-1) marker).
 FT /FTid=VAR_003887.
 FT L -> M (in G1M(non-1) marker).
 FT /FTid=VAR_003888.
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 23 24
 FT STRAND 26 33
 FT STRAND 38 38
 FT STRAND 41 41
 FT TURN 42 45
 FT TURN 48 49
 FT STRAND 50 52
 FT STRAND 57 58
 FT TURN 59 61
 FT STRAND 62 71
 FT HELIX 73 75
 FT TURN 76 78
 FT STRAND 82 87
 FT TURN 88 91
 FT STRAND 92 97
 FT TURN 102 103
 FT STRAND 122 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 149
 FT STRAND 157 162
 FT TURN 163 164
 FT STRAND 165 167
 FT STRAND 171 172
 FT STRAND 176 177
 FT TURN 179 180
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 207
 FT TURN 209 210
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT STRAND 238 242
 FT STRAND 245 256
 FT STRAND 261 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 311
 FT TURN 313 314
 FT HELIX 316 318
 FT STRAND 319 324
 FT SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
 Query Match 53.2%; Score 1204; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 4.2e-71;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 183 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEV 242
 DB 108 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEV 167

QY 243 HNAKTPREQYNSTRVSVLTCLVKGFPYPSDIAVWESNGQPNKYKTPPVLDSDGSP 302
 DB 168 HNAKTPREQYNSTRVSVLTCLVKGFPYPSDIAVWESNGQPNKYKTPPVLDSDGSP 227
 QY 303 EPOVYTLPPSRDELTKNQVSLTCLVKGFPYPSDIAVWESNGQPNKYKTPPVLDSDGSP 362
 DB 228 EPOVYTLPPSRDELTKNQVSLTCLVKGFPYPSDIAVWESNGQPNKYKTPPVLDSDGSP 287
 QY 363 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 404
 DB 288 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 329

RESULT 2
 Q6GMX6 PRELIMINARY; PRT; 465 AA.
 AC Q6GMX6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Klausner R.D., Collins F.S., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Casavant T.L., Scheetz T.E.,
 Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073766; AAH73766.1; -;
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 4.
 DR SMART; SM00409; IGcl; 3.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PSS0835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 465 AA; B3A9B7D0FDB1386E CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 465;
 Best Local Similarity 100.0%; Pred. No. 6.2e-71;

Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 TCPPCPAPELLGGPSVFLPPPKKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
 DB 243 TCPPCPAPELLGGPSVFLPPPKKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 302
 QY 243 HNAKTPREQYNSTRVSVLTCLVKGFPYPSDIAVWESNGQPNKYKTPPVLDSDGSP 302
 DB 303 HNAKTPREQYNSTRVSVLTCLVKGFPYPSDIAVWESNGQPNKYKTPPVLDSDGSP 362
 QY 303 EPOVYTLPPSRDELTKNQVSLTCLVKGFPYPSDIAVWESNGQPNKYKTPPVLDSDGSP 362
 DB 363 EPOVYTLPPSRDELTKNQVSLTCLVKGFPYPSDIAVWESNGQPNKYKTPPVLDSDGSP 422
 QY 363 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 404
 DB 423 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 464

RESULT 3
 Q6IN78 PRELIMINARY; PRT; 466 AA.
 AC Q6IN78;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Casavant T.L., Scheetz T.E.,
 Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC072419; AAH72419.1; -;
 DR HSSP; P01861; 1ADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG LIKE; 4.

DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
 SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCBDE81076E CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 466;
 Best Local Similarity 100.0%; Pred. No. 6.2e-71;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
 DB 244 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 303
 QY 243 HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEITISKAKGQPR 302
 DB 304 HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEITISKAKGQPR 363
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSF 362
 DB 364 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSF 423
 QY 363 FLYSKLTVDSRWQOQGNVFCSCVMHEALHNHYTKQSLSPG 404
 DB 424 FLYSKLTVDSRWQOQGNVFCSCVMHEALHNHYTKQSLSPG 465

RESULT 4

Q727P5 ID Q727P5 PRELIMINARY; PRT; 469 AA.
 AC Q727P5
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE IGH1 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC051328; AAH51328.1; --
 DR HSSP; P01857; 1HZH.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00406; Igv; 1.

DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
 SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 469;
 Best Local Similarity 100.0%; Pred. No. 6.3e-71;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
 DB 247 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 306
 QY 243 HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEITISKAKGQPR 302
 DB 307 HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEITISKAKGQPR 366
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSF 362
 DB 367 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSF 426
 QY 363 FLYSKLTVDSRWQOQGNVFCSCVMHEALHNHYTKQSLSPG 404
 DB 427 FLYSKLTVDSRWQOQGNVFCSCVMHEALHNHYTKQSLSPG 468

RESULT 5

Q6PUA4 ID Q6PUA4 PRELIMINARY; PRT; 470 AA.
 AC Q6PUA4
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018747; AAH18747.1; --
 DR HSSP; P01861; 1ADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_v.
 DR InterPro; IPR003596; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein_Unknown_2.
 SQ SEQUENCE 470 AA; 51715 MW; 7849556A11FD7D99 CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 470;
 Best Local Similarity 100.0%; Pred. No. 6.3e-71;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 242
 DB 248 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 307
 QY 243 HNAKTKPREEQYNSTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 302
 DB 308 HNAKTKPREEQYNSTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 367
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 362
 DB 368 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 427
 QY 363 FLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
 DB 428 FLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 469

RESULT 6

Q725W1 PRELIMINARY; PRT; 470 AA.

ID Q725W1
 AC Q725W1
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udín T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC053984; AAH53984.1; -;
 DR HSSP; P01857; 1H2H.

DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 470;
 Best Local Similarity 100.0%; Pred. No. 6.3e-71;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 242
 DB 248 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 307
 QY 243 HNAKTKPREEQYNSTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 302
 DB 308 HNAKTKPREEQYNSTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 367
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 362
 DB 368 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 427
 QY 363 FLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
 DB 428 FLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 469

RESULT 7

Q6N089 PRELIMINARY; PRT; 472 AA.

ID Q6N089
 AC Q6N089
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686P15220.
 GN Name=DKFZp686P15220;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RG The German Human cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640627; CAE45781.1; -;
 DR HSSP; P01861; 1ADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 6.3e-71;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 242

```

Db 250 TCPPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 309
Qy 243 HNAKTKPREEQYNSTYRVWSVLTVLHQDLWNGKEYCKVSNKALPAPIETKISKAKQPR 302
Db 310 HNAKTKPREEQYNSTYRVWSVLTVLHQDLWNGKEYCKVSNKALPAPIETKISKAKQPR 369
Qy 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 362
Db 370 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 429
Qy 363 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 404
Db 430 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 471

RESULT 8
Q6GMW7 ID Q6GMW7 PRELIMINARY; PRT; 475 AA.
AC Q6GMW7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

```

```

Query Match 53.2%; Score 1204; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 6.4e-71;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 TCPPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
Db 253 TCPPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 312
Qy 243 HNAKTKPREEQYNSTYRVWSVLTVLHQDLWNGKEYCKVSNKALPAPIETKISKAKQPR 302
Db 313 HNAKTKPREEQYNSTYRVWSVLTVLHQDLWNGKEYCKVSNKALPAPIETKISKAKQPR 372
Qy 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 362
Db 373 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 432
Qy 363 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 404
Db 433 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 474

RESULT 9
Q6GMX1 ID Q6GMX1 PRELIMINARY; PRT; 476 AA.
AC Q6GMX1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.

```

DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
 Query Match 53.2%; Score 1204; DB 2; Length 476;
 Best Local Similarity 100.0%; Pred. No. 6.4e-71;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 TCPCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
 Db 254 TCPCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 313
 QY 243 HNAKTKPREEQNSTYRVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302
 Db 314 HNAKTKPREEQNSTYRVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 373
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 362
 Db 374 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 433
 QY 363 FLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTKQSLSLSPG 404
 Db 434 FLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTKQSLSLSPG 475
 RESULT 10
 ID Q96P08 PRELIMINARY; PRT; 679 AA.
 AC Q96P08;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Factor VII active site mutant immunoconjugate.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
 RA Hu Z., Garen A.;
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
 cells for immunotherapy in mouse models of prostatic cancer."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu Z., Garen A.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF272774; AAK58686.2; -.
 DR HSSP; P08709; 1KLI.
 DR GO; GO:003576; C:extracellular; IEA.
 DR GO; GO:005509; F:calcium ion binding; IEA.
 DR GO; GO:008233; F:peptidase activity; IEA.
 DR GO; GO:004295; F:proteolysis and peptidolysis; IEA.
 DR GO; GO:006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Asx hydroxyl S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR062209; EGF_Like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR01254; Peptidase s1.
 DR InterPro; IPR009003; Pept Ser_Cys.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF07654; Cl-set; 2.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00407; IGC1; 1.

DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00835; IG_Like; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;
 Query Match 53.2%; Score 1204; DB 2; Length 679;
 Best Local Similarity 100.0%; Pred. No. 9.5e-71;
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 TCPCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
 Db 457 TCPCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 516
 QY 243 HNAKTKPREEQNSTYRVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302
 Db 517 HNAKTKPREEQNSTYRVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 576
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 362
 Db 577 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 636
 QY 363 FLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTKQSLSLSPG 404
 Db 637 FLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTKQSLSLSPG 678
 RESULT 11
 ID Q6P055 PRELIMINARY; PRT; 473 AA.
 AC Q6P055;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]


```

RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match      53.0%; Score 1200; DB 2; Length 473;
Best Local Similarity 99.5%; Pred. No. 1.2e-70;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
Db 251 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 310
QY 243 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302
Db 311 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 370
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 362
Db 371 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 430
QY 363 FLYSKLTVDKSRWQGNVFSCSVHMEALHNHYTQKSLSLSPG 404
Db 431 FLYSKLTVDKSRWQGNVFSCSVHMEALHNHYTQKSLSLSPG 472

RESULT 12
Q6MZQ6 PRELIMINARY; PRT; 475 AA.
ID Q6MZQ6
AC Q6MZQ6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFp686G11190.
GN Name=DKFp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247FD3D35AEC18 CRC64;

Query Match      53.0%; Score 1200; DB 2; Length 480;
Best Local Similarity 99.5%; Pred. No. 1.2e-70;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
Db 258 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 317
QY 243 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302
Db 318 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 377

```

```

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match      53.0%; Score 1200; DB 2; Length 475;
Best Local Similarity 99.5%; Pred. No. 1.2e-70;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
Db 253 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 312
QY 243 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302
Db 313 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 372
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 362
Db 373 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 432
QY 363 FLYSKLTVDKSRWQGNVFSCSVHMEALHNHYTQKSLSLSPG 404
Db 433 FLYSKLTVDKSRWQGNVFSCSVHMEALHNHYTQKSLSLSPG 474

RESULT 13
Q6N094 PRELIMINARY; PRT; 480 AA.
ID Q6N094
AC Q6N094
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFp686O01196.
GN Name=DKFp686O01196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAE45776.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247FD3D35AEC18 CRC64;

Query Match      53.0%; Score 1200; DB 2; Length 480;
Best Local Similarity 99.5%; Pred. No. 1.2e-70;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
Db 258 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 317
QY 243 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302
Db 318 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 377

```

QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 362
 DB 378 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 437
 QY 363 FLYSKLTVDKSRWQOQGVNFSCSVMHGLHHNYTKQSLSLSPG 404
 DB 438 FLYSKLTVDKSRWQOQGVNFSCSVMHGLHHNYTKQSLSLSPG 479

RESULT 14

Q6N097 ID Q6N097 PRELIMINARY; PRT; 481 AA.
 AC Q6N097;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKF2p686H20196.
 GN Name=DKF2p686H20196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RG The German Human cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640619; CAE45773.1; -;
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IGV; 1.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 481 AA; 52759 MW; 47220D9B64BDF98B CRC64;

Query Match 53.0%; Score 1200; DB 2; Length 481;
 Best Local Similarity 99.5%; Pred. No. 1.2e-70;
 Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
 DB 259 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 318
 QY 243 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302
 DB 319 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 378
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 362
 DB 379 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 438
 QY 363 FLYSKLTVDKSRWQOQGVNFSCSVMHGLHHNYTKQSLSLSPG 404
 DB 439 FLYSKLTVDKSRWQOQGVNFSCSVMHGLHHNYTKQSLSLSPG 480

RESULT 15

Q7Z351 ID Q7Z351 PRELIMINARY; PRT; 482 AA.
 AC Q7Z351;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein DKF2p686N02209.
 GN Name=DKF2p686N02209;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX538118; CAD98026.1; -;
 DR HSSP; P01857; IZH.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00407; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;

Query Match 53.0%; Score 1200; DB 2; Length 482;
 Best Local Similarity 99.5%; Pred. No. 1.2e-70;
 Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
 DB 260 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 319
 QY 243 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302
 DB 320 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 379
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 362
 DB 380 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 439
 QY 363 FLYSKLTVDKSRWQOQGVNFSCSVMHGLHHNYTKQSLSLSPG 404
 DB 440 FLYSKLTVDKSRWQOQGVNFSCSVMHGLHHNYTKQSLSLSPG 481

Search completed: March 8, 2005, 14:44:40
 Job time : 75.6958 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:11 ; Search time 84.1064 Seconds
(without alignments)
1843.986 Million cell updates/sec

Title: US-09-389-782a-8
Perfect score: 2246
Sequence: 1 MKHTCPCPAPPELLGGRS.....QKGNATHDNCNSENSTOK 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2246	100.0	401	4	AAB80904 Human met
2	2246	100.0	401	4	AAY72922 Human met
3	1271.5	56.6	613	8	ADR46827 Human bet
4	1271.5	56.6	861	7	ADG76139 Human NOV
5	1271.5	56.6	861	8	ADF45362 Human sem
6	1271.5	56.6	861	8	ADO40296 Human sem
7	1271.5	56.6	878	7	ADG76141 Human NOV
8	1271.5	56.6	878	8	ADF45364 Human sem
9	1271.5	56.6	878	8	ADO40298 Human sem
10	1254.5	55.9	409	7	ADP75170 Fusion co
11	1249	55.6	731	4	AAMS2156 Humanised
12	1249	55.6	741	4	AAMS2159 Humanised
13	1244	55.4	412	7	ADP75168 Fusion co
14	1241	55.3	489	7	ADC98610 Human ang
15	1240	55.2	248	3	AAB17951 FC-TNF-al
16	1240	55.2	248	5	ABB73419 FC-TNF-al
17	1239	55.2	652	2	AAW48650 Heavy cha
18	1239	55.2	406	7	ADP75162 Fusion co
19	1239	55.2	409	7	ADP75176 Fusion co
20	1239	55.2	410	7	ADP75166 Fusion co
21	1239	55.2	416	7	ADP75164 Fusion co
22	1239	55.2	416	7	ADP75160 Fusion co
23	1239	55.2	422	7	ADP75174 Fusion co
24	1239	55.2	450	7	ADP75172 Fusion co
25	1238	55.1	228	3	AAY96529 Human Igg

26	1238	55.1	228	3	AAB16955 Human Igg
27	1238	55.1	228	4	AAB98953 Human Igg
28	1238	55.1	228	5	ABB04279 Human Igg
29	1238	55.1	228	5	AAU81074 Human Igg
30	1238	55.1	228	5	AAE14310 Human imm
31	1238	55.1	228	5	ABB73410 Human imm
32	1238	55.1	228	5	AAE66012 Human imm
33	1238	55.1	228	5	AAU73018 Human imm
34	1238	55.1	228	6	ABJ38267 Human Igg
35	1238	55.1	228	7	ADN59683 Human Igg
36	1238	55.1	228	8	ADM17708 Human Igg
37	1238	55.1	228	8	ADG75329 Human Igg
38	1238	55.1	243	3	AAB17957 FC-MMP in
39	1238	55.1	243	5	ABB73425 FC-MMP in
40	1238	55.1	243	7	ADN59746 Vector 20
41	1238	55.1	247	3	AAB16958 FC-TMP pr
42	1238	55.1	247	5	ABB73411 FC-TPO mi
43	1238	55.1	248	3	AAB17953 FC-IL-1 a
44	1238	55.1	248	5	ABB73421 FC-interl
45	1238	55.1	250	7	ADD31616 Ang-2 pep

ALIGNMENTS

RESULT 1
AAB80904
ID AAB80904 standard; protein; 401 AA.
XX AAB80904;
AC AAB80904;
XX 31-MAY-2001 (first entry)
XX Human metFcDeltaC-OPG(22-194) fusion protein.

XX Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
XX multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
XX osteoclast formation inhibition; bone resorption inhibition;
XX immunoglobulin.

XX Homo sapiens.
XX WO200117543-A2.
XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-US022806.
XX 03-SEP-1999; 99US-00389545.
XX (AMGE-) AMGEN INC.

XX Dunstan CR;
XX WPI; 2001-265936/27.

XX Preventing or treating lytic bone diseases, particularly associated with cancer or metastasis, by administering an osteoprotegrin polypeptide.
XX Claim 11; Fig 8; 87pp; English.

XX The present invention relates to a method for the prevention or treatment of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypeptide or OPG fusion protein. The present sequence is one such OPG fusion protein. OPG inhibits formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The OPG polypeptide can be used in a method of preventing or treating lytic bone disease, for preventing metastasis of cancer to bone (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal, rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal tract, multiple myeloma or lymphoma) and preventing the osteosclerotic

CC bone metastasis. The OPG fusion polypeptides are used in the prevention
CC or treatment of loss of bone mass, which occurs in conditions including
CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
CC congenital forms of osteoporosis (osteogenesis imperfecta,
CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
CC due to immobilisation of extremities; Paget's disease of bone (osteitis
CC deformans) in adults and juveniles; osteomyelitis, or an infectious
CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
CC hyperthyroidism and renal function disorders; osteopaenia following
CC surgery, induced by steroid administration, and associated with disorders
CC of the small and large intestine and with chronic hepatic and renal
CC diseases; osteonecrosis, or bone cell death, associated with traumatic
CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
CC cell anaemia, systemic lupus erythematosus and other conditions; bone
CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
CC are also used in the replacement of structurally sound bone with
CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
CC in adults and juveniles; hyperparathyroidism, in congenital bone
CC disorders such as fibrous dysplasia, and in osteosclerotic bone
CC metastases. The OPG fusion proteins can exhibit increased circulating
CC half-lives and slower clearance times, thereby providing a more sustained
CC activity. The OPG fusion protein comprises a fragment of the human OPG
CC protein and the FC region of immunoglobulin IgGgamma1 (the hinge, CH2 and
CC CH3 regions; see AAB80897-8)

XX SQ Sequence 401 AA;

Query Match 100.0%; Score 2246; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.4e-140;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCTPCPAPPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCTPCPAPPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQQDLNGKEYCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQQDLNGKEYCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQOGNPFSCVMHEALHNHYTQKSLSLSPGKETFPFKYLHYDE 240
DB 181 SDGSFFLYSKLTVDKSRWQOGNPFSCVMHEALHNHYTQKSLSLSPGKETFPFKYLHYDE 240
QY 301 KQECNRNTRVCEKGRVLEIFCLKHSRCPGFGVQAGTPPENVTKRCPCDGFPSNE 360
DB 301 KQECNRNTRVCEKGRVLEIFCLKHSRCPGFGVQAGTPPENVTKRCPCDGFPSNE 360
QY 361 TSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQK 401
DB 361 TSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQK 401

RESULT 2
AAY72922
ID AAY72922 standard; protein; 401 AA.
XX
AC AAY72922;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human met-Fc (lacking 1-5 residues)-OPG (22-194 aa) fusion protein.

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
KW periodontal.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT 1..228
FT /note= Met-human IgG1 Fc region lacking 1-5 residues;
FT Corresponds to 6-231 residues of human IgG1 Fc region
FT 229..401
FT Region /note= "Derived from human osteoprotegerin fragment (22-
FT 194 residues)"
XX WO200118203-A1.
XX 15-MAR-2001.
XX 18-AUG-2000; 2000WO-US022797.
XX 03-SEP-1999; 99US-00389782.
XX (AMGE-) AMGEN INC.
XX Dunstan CR, Wooden SK, Mann MB;
XX WPI; 2001-244572/25.
XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
XX by e.g. osteoporosis, Paget's disease and osteomyelitis.
XX Claim 7; Fig 8; 119pp; English.

The present sequence is a fusion protein comprising human met-Fc region
(lacking 1-5 residues) which is fused with a sequence derived from human
osteoprotegerin (OPG; 22-194 residues) by a linker. OPG negatively
regulates the formation of osteoclasts in vitro and in vivo. It blocks
the differentiation of osteoclasts from monocyte or macrophage precursors
and the reabsorption of bone. The OPG-Fc fusion protein is administered
for the treatment of bone loss resulting from osteoporosis, Paget's
disease, osteomyelitis, hypercalcaemia, osteonecrosis associated with
surgery or steroid administration, osteonecrosis, bone loss due to
rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or
prosthetic loosening

XX SQ Sequence 401 AA;

Query Match 100.0%; Score 2246; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.4e-140;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCTPCPAPPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCTPCPAPPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQQDLNGKEYCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQQDLNGKEYCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQOGNPFSCVMHEALHNHYTQKSLSLSPGKETFPFKYLHYDE 240
DB 181 SDGSFFLYSKLTVDKSRWQOGNPFSCVMHEALHNHYTQKSLSLSPGKETFPFKYLHYDE 240
QY 241 ETSHQLLCDKCPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECLYCSVPCKELQYV 300
DB 241 ETSHQLLCDKCPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECLYCSVPCKELQYV 300

QY 301 KQSCNTHNRVCKRGYRLEIEFCLKHSRCPGFGVQAGTPTNVTCKRCPDGFPSNE 360
 DB 301 KQSCNTHNRVCKRGYRLEIEFCLKHSRCPGFGVQAGTPTNVTCKRCPDGFPSNE 360
 QY 361 TSSKAPCRKHTNCSVFGLLLTQGNATHDNCISGNSSESTOK 401
 DB 361 TSSKAPCRKHTNCSVFGLLLTQGNATHDNCISGNSSESTOK 401

RESULT 3

AD46827
 ID AD46827 standard; protein; 613 AA.

AC AD46827;
 XX

DT 18-NOV-2004 (first entry)
 XX

DE Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.

XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
 KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 KW betahCG; beta chorionic gonadotropin; antibody;
 KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
 KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 KW antibody B11; betahCG-B11 molecular conjugate; fusion protein.

XX Homo sapiens.
 OS Synthetic.

OS WO2004074432-A2.

XX PD 02-SEP-2004.

XX PF 30-JAN-2004; 2004WO-US0002725.

XX PR 31-JAN-2003; 2003US-0443979P.

XX PA (MEDA-) MEDAREX INC.

XX PI Keler T, Endres M, He L, Ramakrishna V;
 XX WPI; 2004-635555/61.

XX DR N-PSDB; AD46826.

XX PT New molecular conjugate having a monoclonal antibody that binds to human
 PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
 PT cytotoxic T cell response in cancers and infectious diseases.

XX Example 1; SEQ ID NO 10; 82pp; English.

XX The present invention describes a molecular conjugate comprising a
 CC monoclonal antibody that binds to human antigen presenting cells (APCs)
 CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
 CC comprises a heavy and/or light chain variable region derived from a human
 CC VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences
 CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
 CC described: (1) a molecular conjugate comprising a human antibody heavy
 CC chain and a human antibody light chain, where either or both chains are
 CC linked to betahCG; (2) a molecular conjugate comprising a human single
 CC chain antibody that binds to human APCs linked to betahCG, where the
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates
 CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances a T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates

CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and a monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either in vivo or ex
 CC vivo with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimalarial activities, and can be used as a CD8 agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancers and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents a human betahCG-B11 molecular
 CC conjugate, which is used in the exemplification of the present invention.

XX SQ Sequence 613 AA;

Query Match 56.6%; Score 1271.5; DB 8; Length 613;
 Best Local Similarity 66.6%; Pred. No. 1.4e-75;

Matches 259; Conservative 18; Mismatches 53; Indels 59; Gaps 8;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61

DB 239 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 298

QY 62 GVEVHNATKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 121

DB 299 GVEVHNATKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 358

QY 122 GQPRSPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLD 181

DB 359 GQPRSPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLD 418

QY 182 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKLSLSGCKETFPKPKYLHYD 241

DB 419 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKLSLSGCKETFPKPKYLHYD 467

QY 242 TSHQLLCKDCPP--GTYLKHQ-----CTAKWKTVCAPCPDHYTDSWHTSDECLYSPVC 294

DB 468 SSKEPLRPRCPINATLAVEKSGCPVITNTICAG-----YCPMT 510

QY 295 KELQVYKQECNTHNRVCKRGYRLEIEFCLKHSRCPGFGVQAGTPTNVTCKR 351

DB 511 RVLQGLPALPQV--VCNRYDVRPESIRL----PGCPRGVNPVWSYVALSCQCALCRR 563

QY 352 -----CPDGFPSNETSSKAP 366

DB 564 STTDCGGPKDHPLTCDPRFQDSSSSKAP 592

RESULT 4

ADG76139

ID ADG76139 standard; protein; 861 AA.

XX ADG76139;

AC ADG76139;

XX 11-MAR-2004 (first entry)

XX Human NOVX protein to treat human pathological conditions (SeqID 52).
 DE human; NOVX; metabolic disorder; diabetes; anorexia; cancer;
 XX human; NOVX; metabolic disorder; diabetes; anorexia; cancer;
 KW cardiovascular; infectious; neurodegenerative; immune;
 KW haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic;
 KW antiinflammatory; neuroprotective; antilipaeamic; anabolic; cardiant;
 KW neurogenesis; wound healing; angiogenesis; chromosome mapping;
 KW tissue typing; preventive medicine; pharmacogenomic.

XX Homo sapiens.

XX WO2003085096-A2.

XX

16-OCT-2003.
01-APR-2003; 2003WO-US009929.
01-APR-2002; 2002US-0368996P.
04-APR-2002; 2002US-0369980P.
05-APR-2002; 2002US-0370381P.
08-APR-2002; 2002US-0370969P.
09-APR-2002; 2002US-0371002P.
12-APR-2002; 2002US-0372002P.
30-MAY-2002; 2002US-0384297P.
07-JUN-2002; 2002US-0386816P.
13-JUN-2002; 2002US-0389123P.
09-AUG-2002; 2002US-0402207P.
24-OCT-2002; 2002US-0420860P.
31-MAR-2003; 2003US-00403676.
(CURA-) CURAGEN CORP.
Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Casman SJ;
Edinger SR, Gerlach VL, Grosse WM, Guo X, Gusev VY, Ji W;
Larochelle WJ, Lepley DM, Li L, Liu X, Macdougall JR, Malyankar UM;
Millet I, Padigaru M, Patturajan M, Peyman JA, Rastelli L;
Rieger DK, Rothenberg ME, Shinkets RA, Stone DJ, Taupier RJ;
Vernet CAM, Zerhusen BD;
WPI; 2003-812726/76.
N-PSDB; ADG76138.
New isolated NOVX polypeptides and polynucleotides, useful for
preventing, diagnosing or treating NOVX-associated disorders, e.g.
osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
asthma, or infections.
Claim 1; SEQ ID NO 52; 324pp; English.
This invention relates to a novel nucleic acids, and encoded polypeptides
thereof, which have properties related to the stimulation of biochemical
or physiological responses in a cell, tissue, organ or organism.
Specifically, it refers to the use of biologically active fragments for
diagnostic and prognostic assays and furthermore in the treatment of
diverse pathological conditions. The present invention describes novel
human and murine NOVX proteins, as well as methods to modulate their
expression using antisense oligos, ribozymes and peptide nucleic acids.
The polypeptides, nucleic acid molecules and antibodies are useful in the
manufacture of a medicament for treating metabolic disorders, diabetes,
anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune
and haematopoietic diseases as well as various dyslipidaemias.
Accordingly, these molecules have many activities including anorectic,
virucide, nootropic, antiinflammatory, neuroprotective, antilipemic,
anabolic and cardiant. Furthermore, they are useful in screening assays
to identify small molecules that modulate or inhibit, for example,
neurogenesis, wound healing and angiogenesis. The nucleic acids are also
used as in chromosome mapping, tissue typing, preventive medicine and
pharmacogenomics. This polypeptide is a human NOVX protein of the
invention.
Sequence 861 AA;
Query Match 56.6%; Score 1271.5; DB 7; Length 861;
Best Local Similarity 63.8%; Pred. No. 2.1e-75;
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;
QY 2 DKHTCCPCPAPELGGPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 1 DKHTCCPCPAPELGGPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60
QY 62 GVEVHNATKPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 121
Db 61 GVEVHNATKPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 120
QY 122 GPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
XX

Db 121 GPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
QY 182 DGSFELYSLKTVDKSRWQGNVFSVMHEALHNNHYTKSLSPGK-----ETFPDPK 234
Db 181 DGSFELYSLKTVDKSRWQGNVFSVMHEALHNNHYTKSLSPGKGGGGGGGFPF- 239
QY 235 YLHYDEE---TSHQLLCKKCPGTYLKQH-----CTAKWK-----TVC 269
Db 240 ----DSEPISSH-----GNTKYQYFVGHKPGNTTORHLDIQIMINWGLY 286
QY 270 APCPDHYT---DSWHTSDECLYCSPVCKELQYVKQECNTRHNVCECK-EGRYLE---- 321
Db 287 TAARDHIYTVDTIDTSTTEE--IYCS---KLTWKSROAD-----VDTCRMKGKHDECHN 336
QY 322 -LEFCLKHSRCPGPGVGVQAGTPENTVCKRC-----PDGFFSNETSKAPC---RQHT 371
Db 337 FIKVLKKND---DALFVCGTNAFNPSCRNYKMDTLEP---FGDFSGMARCPYDAKHA 389
QY 372 NCSVF 376
Db 390 NVALF 394
RESULT 5
ADF45362
ID ADF45362 standard; protein; 861 AA.
XX AC ADF45362;
XX AC ADF45362;
DT 26-FEB-2004 (first entry)
XX DE Human semaphorin-like protein NOV2t protein SEQ ID NO:52.
XX KW cell migration inhibition; semaphorin-like protein;
KW angiogenesis inhibition; actin filament formation inhibition;
KW angiogenic related disorder; cytostatic; gene therapy; cancer;
KW neuroblastoma; renal carcinoma; fibrosarcoma; rhabdosarcoma cell;
KW pancreatic cancer; human.
OS Homo sapiens.
XX WO2003102584-A2.
XX PD 11-DEC-2003.
XX PF 30-MAY-2003; 2003WO-US017412.
XX PR 30-MAY-2002; 2002US-0384798P.
XX PR 09-AUG-2002; 2002US-0402407P.
XX PR 28-JAN-2003; 2003US-0443062P.
XX PR 31-MAR-2003; 2003US-00403676.
XX PA (CURA-) CURAGEN CORP.
XX PI Alvarez E, Anderson DW, Dhanabal M, Khrantsov NV, Larochelle WJ;
PI Lichenstein HS, Li L, Ooi CE, Padigaru M, Shinkets RA, Zhong M;
XX DR WPI; 2004-035474/03.
XX DR N-PSDB; ADF45361.
PT Inhibiting cell migration, useful in diagnosing and treating disorders
PT such as cancer, e.g. neuroblastoma, renal carcinoma, fibrosarcoma or
PT rhabdosarcoma, by contacting a cell with a composition comprising NOVX
PT polypeptide.
XX Claim 1; SEQ ID NO 52; 197pp; English.
XX The present invention describes a method for inhibiting cell migration
XX which comprises contacting a cell with a composition comprising a
XX polypeptide (I) having at least 95% sequence identity to any of the 22
XX sequences of 17-1047 amino acids (SVEN SEQ ID NOS: 14-56) or any of the
XX 22 sequences of 51-4250 base pairs (ODD SEQ ID NOS: 13-55) defined in the
XX specification, where (I) is a semaphorin-like protein. Also described:

CC (1) a method of inhibiting angiogenesis of a tissue; (2) a method of
CC inhibiting actin filament formation in a cell; (3) a method of preventing
CC or alleviating a symptom of an angiogenic related disorder; (4) a
CC chimeric protein comprising a first polypeptide (1) and second
CC polypeptide; and (5) a composition comprising a sequence of 649 or 878
CC amino acids (see ADF45360 or ADF45364). (1) has cytostatic activity, and
CC can be used in gene therapy. The method is useful for inhibiting cell
CC migration. (1) and the polynucleotides encoding them can be used in
CC diagnosing and treating disorders such as cancer, e.g. neuroblastoma,
CC renal carcinoma, fibrosarcoma, rhabdomyosarcoma cell or a pancreatic cancer.
CC The present sequence is used in the exemplification of the present
CC invention.

XX Sequence 861 AA;

Query Match 56.6%; Score 1271.5; DB 8; Length 861;
Best Local Similarity 63.8%; Pred. No. 2.1e-75;
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 1 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60
QY 62 GVEVHNKTPREBQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 61 GVEVHNKTPREBQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
DB 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
QY 182 DGSFFLYSKLTVDKSRWQGNVSCSWMEALHNNHYTKLSLSPGK-----ETFPKP 234
DB 181 DGSFFLYSKLTVDKSRWQGNVSCSWMEALHNNHYTKLSLSPGKGGGGGGGFPPE- 239
QY 235 YLHYDES---TSQLLCDKCPGGYLLKOH-----CTAKWK-----TVC 269
DB 240 ----DSEPISSH-----GNYTKQYVFGVGHKPGRTTQRHLDIQIMIMNGTLY 286
QY 270 APCPDHYTT---DSWHTSDECLYCSPVKELQYVQECNTRNRCBCK-EGRYLE---- 321
DB 287 IAARDHIYTVIDTSHTEE--IYCS---KGLTKWSRQAD-----VDTCRMKGKHKBCHN 336
QY 322 -ISFCLKHSRCPGFGVQAGTERTNVTCKRC-----PDGFFSNETSSAPC---RKHT 371
DB 337 FIKVLLKKNL-----DALFVCGTNAFNSCRNYKMDTLEP---FGDFPSGNMRCFYDAKHA 389
QY 372 NCSVF 376
DB 390 NVALF 394

RESULT 6

ADO40296
ID ADO40296 standard; protein; 861 AA.

XX ADO40296;

XX 15-JUL-2004 (first entry)

DE Human semaphorin-like protein NOV2t.

XX Human; semaphorin; NOV2; angiogenesis inhibitor; gene therapy;
KW cell migration; angiogenesis; actin filament formation;
KW angiogenic-related disorder; loss of balance; weight loss; slow speech;
KW jaundice; fatigue; pain; blood in urine; anaemia; swollen bone; cancer;
KW pancreatic cancer; renal cancer; neuroblastoma; wound healing;
KW tissue regeneration.

XX Homo sapiens.

XX US2004018977-A1.

XX

PD 29-JAN-2004.

XX 30-MAY-2003; 2003US-00449548.

XX 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-00520781.

PR 09-APR-2002; 2002US-0371002P.

PR 30-MAY-2002; 2002US-0384798P.

PR 09-AUG-2002; 2002US-0402407P.

PR 28-JAN-2003; 2003US-0443062P.

PR 31-MAR-2003; 2003US-00403676.

XX (ALVA/) ALVAREZ E.

PA (ANDE/) ANDERSON D W.

PA (DHAN/) DHANABAL M.

PA (KHRA/) KHRAMTSOV N V.

PA (LARO/) LAROCHELLE W J.

PA (LICH/) LICHENSTEIN H S.

PA (LILL/) LI L.

PA (OOIC/) OOI C E.

PA (PADL/) PADIGARU M.

PA (SHIM/) SHIMKETS R A.

PA (ZHON/) ZHONG M.

XX Alvarez E, Anderson DW, Dhanabal M, Khrantsov NV, Larochelle WJ;

PI Lichenstein HS, Li L, Ooi CE, Padigaru M, Shimkets RA, Zhong M;

XX WPI; 2004-122082/12.

DR N-PSDB; ADO40295.

XX Inhibiting cell migration, angiogenesis of a tissue or actin filament
PT formation in a cell, for preventing or treating cancer, e.g. renal
PT cancer, comprises contacting or introducing a semaphorin-like polypeptide
PT or nucleic acid.

XX Claim 1; SEQ ID NO 52; 227pp; English.

XX The invention relates to inhibiting cell migration, angiogenesis of a
CC tissue or actin filament formation in a cell comprising contacting the
CC cell with a composition comprising a semaphorin-like polypeptide having
CC at least 95 % sequence identity to any one of 22 NOV2 (NOVA-NOVU)
CC proteins (appearing as ADO40258, ADO40260, ADO40262, ADO40264, . . . etc to
CC ADO40300), or introducing to a cell a composition comprising a nucleic
CC acid having at least 95 % sequence identity to any one of the 22 nucleic
CC acids encoding the NOV2 proteins (appearing as ADO40257, ADO40259,
CC ADO40261, ADO40263, . . . etc to ADO40299). Also included are preventing or
CC alleviating a symptom of an angiogenic-related disorder comprising
CC administering to a subject a composition comprising the semaphorin-like
CC polypeptide cited above, a chimeric protein comprising a first
CC polypeptide comprising a NOV2 polypeptide and second polypeptide, and a
CC composition comprising a NOV2s (ADO40294) or NOV2u (ADO40298). The
CC semaphorin-like proteins or nucleic acids are useful for inhibiting cell
CC migration, angiogenesis of a tissue or actin filament formation, or for
CC diagnosing, preventing and treating an angiogenic-related disorder (with
CC symptoms such as loss of balance, weight loss, slow speech, jaundice,
CC fatigue, pain, blood in urine, anaemia or swollen bones) such as cancer,
CC e.g. pancreatic cancer, renal cancer or neuroblastoma, wound healing and
CC tissue regeneration. The nucleic acid may be used in gene therapy. The
CC present sequence represents a NOV2, semaphorin-like protein.

XX Sequence 861 AA;

Query Match 56.6%; Score 1271.5; DB 8; Length 861;
Best Local Similarity 63.8%; Pred. No. 2.1e-75;
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61

DB 1 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60

QY 62 GVEVHNKTPREBQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121

DB 61 GVEVHNKTPREBQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120

Qy 122 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDL 181
Db 121 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDL 180
Qy 182 DGSFFLYSLKTVDKSRWQOGNVFSCSVWHEALHNYTKSLSPGK-----ETFPK 234
Db 181 DGSFFLYSLKTVDKSRWQOGNVFSCSVWHEALHNYTKSLSPGKGGGGGGGPF- 239
Qy 235 YLHYDEE---TSHQLLCKDPCPGYLLKQH-----CTAKWK-----TVC 269
Db 240 ----DSEPIISH-----GNYTKQYPVFVGHKPGRNTTQRHLDIQIMIMNGTLY 286
Qy 270 APCPDHYVT---DSWHTSDECLYCSPVCKELQVVKQECNRTHRVCECK-EGRYLE---- 321
Db 287 IAARDHIYTVDDIDTSHTEE---IYCS---KKLTWKSQAD-----VDCRMKGKDECHN 336
Qy 322 -IEFCLKHSRCPGFGVVGAGTPERNTVCRC-----PDGFFSNSTSSKAPC---RKHT 371
Db 337 FIKVLLKND-----DALFVCGTNAFNPSCRNYKMDTLEP---FGDEFSGMARCFYDAKHA 389
Qy 372 NCSVF 376
Db 390 NVALF 394

RESULT 7
ID ADG76141
AC ADG76141 standard; protein; 878 AA.

XX ADG76141;

DT 11-MAR-2004 (first entry)

DE Human NOVX protein to treat human pathological conditions (SeqID 54).
XX human; NOVX; metabolic disorder; diabetes; anorexia; cancer;
KW cardiovascular; infectious; neurodegenerative; immune;
KW haematopoietic disease; dyslipidaemia; anorectic; virucide; neurotropic;
KW antiinflammatory; neuroprotective; antilipaeamic; anabolic; cardiac;
KW neurogenesis; wound healing; angiogenesis; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic.

XX Homo sapiens.

PN WO2003085096-A2.

XX 16-OCT-2003.

PF 01-APR-2003; 2003WO-US009929.

XX 01-APR-2002; 2002US-0368996P.

PR 04-APR-2002; 2002US-0369980P.

PR 05-APR-2002; 2002US-0370381P.

PR 08-APR-2002; 2002US-0370969P.

PR 09-APR-2002; 2002US-0371002P.

PR 12-APR-2002; 2002US-0372002P.

PR 30-MAY-2002; 2002US-0384297P.

PR 07-JUN-2002; 2002US-0386816P.

PR 13-JUN-2002; 2002US-0389123P.

PR 09-AUG-2002; 2002US-0402207P.

PR 24-OCT-2002; 2002US-0420860P.

PR 31-MAR-2003; 2003US-0040367P.

XX (CURA-). CURAGEN CORP.

PA Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Casman SJ;

PI Edinger SR, Gerlach VL, Grose WM, Guo X, Gusev YV, Ji W;

PI Larochelle WJ, Lepley DM, Li L, Liu X, Macdougall JR, Malyankar UM;

PI Millet I, Padigaru M, Patturajan M, Peyman JA, Rastelli L;

PI Rieger DK, Rothenberg MB, Shinkets RA, Stone DJ, Taupier RJ;

PI Vernet CAM, Zerhusen BD;

DR WPI; 2003-812726/76.
XX N-PSDB; ADG76140.
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
PS Claim 1; SEQ ID NO 54; 324pp; English.

XX This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The polypeptides, nucleic acid molecules and antibodies are useful in the
CC manufacture of a medicament for treating metabolic disorders, diabetes,
CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune
CC and haematopoietic diseases as well as various dyslipidaemias.
CC Accordingly, these molecules have many activities including anorectic,
CC virucide, neurotropic, antiinflammatory, neuroprotective, antilipaeamic,
CC anabolic and cardiac. Furthermore, they are useful in screening assays
CC to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.

XX Sequence 878 AA;

Qy Query Match 56.6%; Score 1271.5; DB 7; Length 878;
Db Best Local Similarity 63.8%; Pred. No. 2.1e-75;
XX Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

Qy 2 DKHTCCPCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61

Db 1 DKHTCCPCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVD 60

Qy 62 GVEVHNATKPREQYNSYTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121

Db 61 GVEVHNATKPREQYNSYTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120

Qy 122 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDL 181

Db 121 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDL 180

Qy 182 DGSFFLYSLKTVDKSRWQOGNVFSCSVWHEALHNYTKSLSPGK-----ETFPK 234

Db 181 DGSFFLYSLKTVDKSRWQOGNVFSCSVWHEALHNYTKSLSPGKGGGGGGGPF- 239

Qy 235 YLHYDEE---TSHQLLCKDPCPGYLLKQH-----CTAKWK-----TVC 269

Db 240 ----DSEPIISH-----GNYTKQYPVFVGHKPGRNTTQRHLDIQIMIMNGTLY 286

Qy 270 APCPDHYVT---DSWHTSDECLYCSPVCKELQVVKQECNRTHRVCECK-EGRYLE---- 321

Db 287 IAARDHIYTVDDIDTSHTEE---IYCS---KKLTWKSQAD-----VDCRMKGKDECHN 336

Qy 322 -IEFCLKHSRCPGFGVVGAGTPERNTVCRC-----PDGFFSNSTSSKAPC---RKHT 371

Db 337 FIKVLLKND-----DALFVCGTNAFNPSCRNYKMDTLEP---FGDEFSGMARCFYDAKHA 389

Qy 372 NCSVF 376

Db 390 NVALF 394

XX RESULT 8

ADG76141

ID ADF45364 standard; protein; 878 AA.

XX ADF45364;
 AC 26-FEB-2004 (first entry)
 XX Human semaphorin-like protein NOV2u protein SEQ ID NO:54.
 DE cell migration inhibition; semaphorin-like protein;
 XX angiogenesis inhibition; actin filament formation inhibition;
 KW angiogenic related disorder; cytostatic; gene therapy; cancer;
 KW neuroblastoma; renal carcinoma; fibrosarcoma; rhabdosarcoma cell;
 KW pancreatic cancer; human.
 XX
 OS Homo sapiens.
 XX WO2003102584-A2.
 PN 11-DEC-2003.
 PD 30-MAY-2003; 2003WO-US017412.
 PP 30-MAY-2002; 2002US-0384798P.
 PR 09-AUG-2002; 2002US-0402407P.
 PR 28-JAN-2003; 2003US-0443062P.
 PR 31-MAR-2003; 2003US-00403676.
 XX (CURA-) CURAGEN CORP.
 PA Alvarez E, Anderson DW, Dhanabal M, Khrantsov NV, Larochele WJ;
 PI Lichenstein HS, Li L, Ooi CE, Padigaru M, Shimkets RA, Zhong M;
 XX WPI; 2004-035474/03.
 DR N-PSDB; ADF45363.
 XX Inhibiting cell migration, useful in diagnosing and treating disorders
 PT such as cancer, e.g. neuroblastoma, renal carcinoma, fibrosarcoma or
 PT rhabdosarcoma, by contacting a cell with a composition comprising NOVX
 PT polypeptide.
 XX Claim 1; SEQ ID NO 54; 197pp; English.
 XX The present invention describes a method for inhibiting cell migration
 CC which comprises contacting a cell with a composition comprising a
 CC polypeptide (I) having at least 95% sequence identity to any of the 22
 CC sequences of 17-1047 amino acids (SVEN SEQ ID NOS: 14-56) or any of the
 CC 22 sequences of 51-4250 base pairs (ODD SEQ ID NOS: 13-55) defined in the
 CC specification, where (I) is a semaphorin-like protein. Also described:
 CC (1) a method of inhibiting angiogenesis of a tissue; (2) a method of
 CC inhibiting actin filament formation in a cell; (3) a method of preventing
 CC or alleviating a symptom of an angiogenic related disorder; (4) a
 CC chimeric protein comprising a first polypeptide (I) and second
 CC polypeptide; and (5) a composition comprising a sequence of 649 or 878
 CC amino acids (see ADF45360 or ADF45364). (I) has cytostatic activity, and
 CC can be used in gene therapy. The method is useful for inhibiting cell
 CC migration. (I) and the polynucleotides encoding them can be used in
 CC diagnosing and treating disorders such as cancer, e.g. neuroblastoma,
 CC renal carcinoma, fibrosarcoma, rhabdosarcoma cell or a pancreatic cancer.
 CC The present sequence is used in the exemplification of the present
 CC invention.
 XX Sequence 878 AA;
 SQ

Query Match
 Best Local Similarity 56.6%; Score 1271.5; DB 8; Length 878;
 Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;
 2 DKTHTCPCPAPLLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
 1 DKTHTCPCPAPLLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60
 62 GVEVHNKTKPREEQNSTYRVVSVLTVLDHQLWNGKEYCKVSKNKPAPTEKTSKAK 121
 61 GVEVHNKTKPREEQNSTYRVVSVLTVLDHQLWNGKEYCKVSKNKPAPTEKTSKAK 120

QY 122 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGPPSDIAVEWESNGQPENNYKTTPPVLD 181
 DB 121 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGPPSDIAVEWESNGQPENNYKTTPPVLD 180
 QY 182 DGSFFLYSKLTVDKSRWQQGNVFCSPVMEALHNHYTQKSLSLSPGK-----ETFPKP 234
 DB 181 DGSFFLYSKLTVDKSRWQQGNVFCSPVMEALHNHYTQKSLSLSPGKGGGGGGGFFE- 239
 QY 235 YLHYDEE---TSHQLLCKDKPPGTLYLKH-----CTAKWK-----TVC 269
 DB 240 ----DSEPISSH-----GNYTKQYVPVGHKPGKGRNTTORHRLDIQIMIMNGTLY 286
 QY 270 APCPDHYIT---DSWHTSDECLYCSPVCKELQVYVQECNRTHNRVCECK-EGRYLE----- 321
 DB 287 IAARDHIYTVDTIDTSHTEB--IYCS---KKLTWKGRQAD-----VDTCRMKGKHKDECHN 336
 QY 322 -IEFCLKHKRSCPPGFGVQAGTPERNVCKRC-----PDGPFNSNETSSKAPC---RKHT 371
 DB 337 FIKVLLKKND----DALFVCGTNAFNPSCRNYKMDTLEP---FGDEFSGMARCPCYDAKHA 389
 QY 372 NCSVF 376
 DB 390 NVALF 394
 RESULT 9
 ADO40298
 ID ADO40298 standard; protein; 878 AA.
 AC ADO40298;
 XX 15-JUL-2004 (first entry)
 DT Human semaphorin-like protein NOV2u.
 DE Human; semaphorin; NOV2; angiogenesis inhibitor; gene therapy;
 KW cell migration; angiogenesis; actin filament formation;
 KW angiogenic-related disorder; loss of balance; weight loss; slow speech;
 KW jaundice; fatigue; pain; blood in urine; anaemia; swollen bone; cancer;
 KW pancreatic cancer; renal cancer; neuroblastoma; wound healing;
 KW tissue regeneration.
 XX Homo sapiens.
 OS US2004018977-A1.
 PN 29-JAN-2004.
 PD 30-MAY-2003; 2003US-00449548.
 PF 09-MAR-1999; 99US-0123667P.
 PR 08-MAR-2000; 2000US-00520781.
 PR 09-APR-2002; 2002US-0371002P.
 PR 30-MAY-2002; 2002US-0384798P.
 PR 09-AUG-2002; 2002US-0402407P.
 PR 28-JAN-2003; 2003US-0443062P.
 PR 31-MAR-2003; 2003US-00403676.
 XX (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.
 XX Alvarez E, Anderson DW, Dhanabal M, Khrantsov NV, Larochele WJ;
 PI Lichenstein HS, Li L, Ooi CE, Padigaru M, Shimkets RA, Zhong M;


```
SQ      Sequence 409 AA;
Query Match      55.9%; Score 1254.5; DB 7; Length 409;
Best Local Similarity 62.3%; Pred. No. 1.1e-74;
Matches 256; Conservative 27; Mismatches 71; Indels 57; Gaps 7;

QY      1 MDKTHCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
16 LDKTHCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 75
QY      61 DGVEVHNAKTKPREEQYNSTYRVSVLTVLIHQDLNKGKEYCKVSNKALPAPIETISKAK 120
DB      76 DGVEVHNAKTKPREEQYNSTYRVSVLTVLIHQDLNKGKEYCKVSNKALPAPIETISKAK 135
QY      121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 180
DB      136 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 195
QY      181 SDGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNHYTQKSLSLSPKETTFFPKYLHYDE 240
DB      196 SDGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNHYTQKSLSLSPKETTFFPKYLHYDE 255
QY      241 -ETSHQLLCDKCPP-GTYLKHCHTAKWKTVCAPCPDHYTDSWHTSDECLYCSPVCKELQ 298
DB      256 PEPEGSLOGDONQIAAHVISEASSKTSVLQWAEKGYTMS----- 297
QY      299 YVQECNRTHNRVCECKEGR-----YLEIEFCLKHRSCTPPGFGVQAGTPERN 346
DB      298 -----NNLVLENGKQLTVKRQGLYIYAQVTFCSNREA-----SSQAPFIA 339
QY      347 TVCKRCPDGF-----FSNETSKAPCRKHTNCSVGLLLTQKGNATHDNI 391
DB      340 SLCLKSPGRFERILLRAANTHSSAKPCGQO-SIHGGVPELOPGASVFNV 389

RESULT 11
AAM52156
ID      AAM52156 standard; protein; 731 AA.
XX      AC
XX      AAM52156;
XX      DT
XX      05-FEB-2002 (first entry)
XX      DE
XX      Humanised HMF-G-1 heavy chain/DNase I fusion protein 1.
XX      KW
XX      Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
XX      KW
XX      cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX      OS
XX      Homo sapiens.
XX      OS
XX      Synthetic.
XX      PN
XX      WO200174905-A1.
XX      PD
XX      11-OCT-2001.
XX      PF
XX      26-MAR-2001; 2001WO-GB001324.
XX      PR
XX      03-APR-2000; 2000GB-00008049.
XX      PR
XX      02-OCT-2000; 2000US-0237159P.
XX      PA
XX      (ANTI-) ANTISOMA RES LTD.
XX      PI
XX      Young RJ;
XX      WPI; 2001-662969/76.
XX      DR
XX      Novel compound used to treat cancer has target cell-specific portion
XX      PT
XX      comprising humanised monoclonal antibody having specificity for
XX      PT
XX      polymorphic epithelial mucin, and cytotoxic portion having
XX      PT
XX      endonucleolytic activity.
XX      PS
XX      Claim 20; Fig 7; 176pp; English.
XX

CC      The invention relates to a compound which comprises a target cell-
CC      specific portion, comprising an humanised monoclonal antibody, having
CC      specificity for polymorphic epithelial mucin (PEM) or its antigen binding
CC      fragment and a cytotoxic portion having endonucleolytic activity.
CC      exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC      compound has cytostatic activity useful for treating cancer and acting as
CC      a potential inducer of apoptosis
XX
SQ      Sequence 731 AA;
Query Match      55.6%; Score 1249; DB 4; Length 731;
Best Local Similarity 65.6%; Pred. No. 5.2e-74;
Matches 254; Conservative 15; Mismatches 56; Indels 62; Gaps 6;

QY      2 DKTHCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB      241 DKTHCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 300
QY      62 GVEVHNAKTKPREEQYNSTYRVSVLTVLIHQDLNKGKEYCKVSNKALPAPIETISKAK 121
DB      301 GVEVHNAKTKPREEQYNSTYRVSVLTVLIHQDLNKGKEYCKVSNKALPAPIETISKAK 360
QY      122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
DB      361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 420
QY      182 DGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNHYTQKSLSLSPKETTFFPKYLHYDEE 241
DB      421 DGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNHYTQKSLSLSPKETTFFPKYLHYDEE 480
QY      242 TSHQLLCDKCPGTYLQK-----HCTAKWK---TVCAFCPDHYV----- 277
DB      481 TFGETKMSNATLVSVIQLSRYDIALVQEVDRDHLTAVGKLLDNLNQADPTDTHYVNSE 540
QY      278 -----TDSWHTSDECLYCSPVCKELQYVQECNRTHNRVCECK 315
DB      541 PLGRNSYKERYLFVYRPDQVSAVDSYVYDDGCEPCG-----NDTFNREPAIV 587
QY      316 E--GRAYLEI-EFCLKHRSCTPPGFGVQ 339
DB      588 RFFSRFTVEVREPAIVPLHAAPGDAVAE 614

RESULT 12
AAM52159
ID      AAM52159 standard; protein; 741 AA.
XX      AC
XX      AAM52159;
XX      DT
XX      05-FEB-2002 (first entry)
XX      DE
XX      Humanised HMF-G-1 heavy chain/DNase I fusion protein 4.
XX      KW
XX      Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
XX      KW
XX      cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX      OS
XX      Homo sapiens.
XX      OS
XX      Synthetic.
XX      PN
XX      WO200174905-A1.
XX      PD
XX      11-OCT-2001.
XX      PF
XX      26-MAR-2001; 2001WO-GB001324.
XX      PR
XX      03-APR-2000; 2000GB-00008049.
XX      PR
XX      02-OCT-2000; 2000US-0237159P.
XX      PA
XX      (ANTI-) ANTISOMA RES LTD.
XX      PI
XX      Young RJ;
XX      WPI; 2001-662969/76.
XX      DR
```

XX Novel compound used to treat cancer has target cell-specific portion
 PT comprising humanized monoclonal antibody having specificity for
 PT polymorphic epithelial mucin, and cytotoxic portion having
 PT endonucleolytic activity.
 XX
 PS Claim 20; Fig 10; 176pp; English.
 XX
 CC The invention relates to a compound which comprises a target cell-
 CC specific portion, comprising an humanised monoclonal antibody, having
 CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding
 CC fragment and a cytotoxic portion having endonucleolytic activity,
 CC exemplified by AAM52154-AAM5168 and encoded by ABA02682-ABA02728. The
 CC compound has cytostatic activity useful for treating cancer and acting as
 CC a potential inducer of apoptosis
 XX
 SQ Sequence 741 AA;
 Query Match 55.6%; Score 1249; DB 4; Length 741;
 Best Local Similarity 65.6%; Pred. No. 5.3e-74;
 Matches 254; Conservative 15; Mismatches 56; Indels 62; Gaps 6;
 QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENNYVD 61
 Db 241 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNYYD 300
 QY 62 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
 Db 301 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360
 QY 122 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
 Db 361 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 420
 QY 182 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPCKETFPKYLHYDEE 241
 Db 421 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPCKGGGKIAAFNIQ 480
 QY 242 TSHQLCDKCPPTGYLKQ-----HCTAKWK---TVCAPCPDHY----- 277
 Db 481 TFGETKMSNATLVSYIVQILSRDYIALVQEVDRDHLTAVGKLLDNLNQADPTVHYVWSE 540
 QY 278 -----TDSWHTSDCLYCSFVCKELQYVQKQCNCNTHNRVCECK 315
 Db 541 PLGRNYSKERYLFVYRPDQVSAVDSYVYDDGCEPCG-----NDTFNREPAIV 587
 QY 316 E--GRYLEI-EFCLKHSRCPGFGVQ 339
 Db 588 RPFSTRTEVREFAIVPLHAAPGDAVAE 614
 RESULT 13
 ADP75168
 ID ADP75168 standard; protein; 412 AA.
 AC ADP75168;
 XX
 DT 12-AUG-2004 (first entry)
 DE Fusion construct psl181 Fc:TNFalpha protein.
 DE
 XX fusion protein; immunoglobulin; Fc region; TNF; tumour necrosis factor;
 KW Fast; TNF-alpha; TNF-gamma; TRAIL; EDAl; EDa2; dermatological;
 KW depilatory; gene therapy; cellular therapy; ectodermal dysplasia;
 KW x-linked immune deficiency; hyper IgM; alopecia; hirsutism; sweat gland;
 KW sebaceous gland.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..15
 FT /note= "HA signal"
 FT

FT Region 18..243
 FT /note= "hlg Fc aa248-473 of g12765420"
 FT Peptide 246..259
 FT /note= "linker peptide"
 FT Region 264..412
 FT /note= "hTNFalpha aa80-228"
 XX
 PN DE10205583-A1.
 XX
 PD 21-AUG-2003.
 XX
 PF 11-FEB-2002; 2002DE-01005583.
 XX
 PR 10-FEB-2002; 2002DE-01005368.
 XX
 PA (APOX-) APOXIS SA.
 XX
 PI Gaide O, Schneider P, Tschopp J;
 XX
 DR WPI; 2003-647319/62.
 DR N-PSDB; ADP75167.
 XX
 PT New recombinant fusion protein, useful for treating deficiency of tumor
 PT necrosis factor ligand, particularly ectodermal dysplasia, comprises the
 PT ligand and immunoglobulin fragment.
 PS
 PS Claim 8; Fig F; 22pp; German.
 XX
 CC This invention describes a novel recombinant fusion protein which
 CC comprises an immunoglobulin Fc segment, the extracellular region of a
 CC tumour necrosis factor (TNF) and optionally a transition region,
 CC including a linker. The TNF ligands used in the method include FasL, TNF-
 CC alpha or TNF-gamma, TRAIL or most preferred, EDAl or 2. The Fc fragment
 CC contains the hinge region and domains CH2 and CH3 of the Fc segment of an
 CC IgG, particularly human. The linker optionally includes a protease
 CC cleavage site. The N-terminus of construct may have a signal sequence,
 CC secretory signal sequence and/or tag (e.g. Flag or His). The products of
 CC the invention have dermatological and depilatory activity. The construct,
 CC or other therapeutic agents, are administered parenterally (especially
 CC intravenously or intra-arterially) during pregnancy, especially as early
 CC as possible, e.g. for humans, in the first 3 months, every second day for
 CC at least 14 days. Nucleic acid encoding the construct, related vectors
 CC and transfected host cells, are useful in gene/cellular therapy of
 CC genetic disorders associated with defective expression of TNF ligand,
 CC particularly ectodermal dysplasia (specifically the X-linked hypohydrotic
 CC form or X-linked immune deficiency with hyper IgM) and also alopecia,
 CC hirsutism and inadequate functioning of the sweat and sebaceous glands.
 CC The fusion protein construct is soluble but still retains ability to
 CC mimic the physiological effects of TNF ligand. This sequence represents
 CC the fusion construct Fc-TNFalpha.
 XX
 SQ Sequence 412 AA;

Query Match 55.4%; Score 1244; DB 7; Length 412;
 Best Local Similarity 64.3%; Pred. No. 5.7e-74;
 Matches 252; Conservative 22; Mismatches 50; Indels 68; Gaps 7;
 QY 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNYY 60
 Db 16 LDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNYY 75
 QY 61 DGEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120
 Db 76 DGEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 135
 QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
 Db 136 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 195
 QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPCKETFPFK----- 234
 Db 196 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPCKRSPQPKPQPK 255

```
QY 235 -----YLHYDEETSHQLLCKCPPTGYLKHQCTAKWKTCAPCPDHYHYTSMHTSDECLY 289
Db 256 PEPESGLQSKPVAH-----VV 272
QY 290 CSPVCK-ELQYVQECNR-----THNRVCECKEGRYL-EIEFCLKHRSCPPGFGVWQ 339
Db 273 ANPAEQGLQWLNRRANALLANGVELRDNLQVVPSEGLYLYSOVLFPKGGC-PSTHVLL 331
QY 340 AGTPERTVCKRCPDGFSSNETSSKAPCRKHT 371
Db 332 THTISRIVSYQTKVNLLS---AIKSPCQRET 360

RESULT 14
ADC98610
ID ADC98610 standard; protein; 489 AA.
XX AC ADC98610;
XX DT 01-JAN-2004 (first entry)
XX DE Human angiogenesis related secreted protein NOV1u SEQ ID NO:44.
XX KW human; angiostatin; secreted protein; angiogenesis;
XX KW fibrinogen binding domain; coiled coil domain; cytoskeletal;
XX KW antiangiogenic; cardiac; vasotrophic; vulnary; osteopathic;
XX KW antirheumatic; antiarthritic; antidiabetic; ophthalmological;
XX KW gene therapy; angiogenesis inhibitor; tumour; tumour metastasis;
XX KW ischaemic heart disease; peripheral vascular disease; wound healing;
XX KW bone repair; rheumatoid arthritis; diabetic retinopathy.
XX OS Homo sapiens.
XX PN WO2003078648-A2.
XX PD 25-SEP-2003.
XX PF 11-MAR-2003; 2003WO-US007586.
XX PR 11-MAR-2002; 2002US-0363266P.
XX PA (CURA-) CURAGEN CORP.
XX PI Dhanabal M, Wu F, Larochele WJ, Lichenstein HS;
XX DR N-PSDB; ADC98609.
XX PT New isolated Angiostatin polynucleotide and polypeptides, useful for
XX PT inhibiting the growth of a tumor, tumor metastasis or angiogenesis, and
XX PT for treating ischemic heart disease, rheumatoid arthritis and diabetic
XX PT retinopathy.
XX PS Claim 3; SEQ ID NO 44; 88pp; English.
XX CC The present invention describes human angiostatin secreted proteins
XX CC having antiangiogenesis activity. More specifically described is an
XX CC isolated polynucleotide (I) encoding a fibrinogen binding domain (FBD)
XX CC and a coiled coil (CC) domain. (I) has cytostatic, antiangiogenic,
XX CC cardiac, vasotrophic, vulnary, osteopathic, antirheumatic, and can be
XX CC antiarthritic, antidiabetic and ophthalmological activities, and can be
XX CC used in gene therapy, and as an angiogenesis inhibitor. Methods and
XX CC compositions of the present invention of inhibiting angiostatin
XX CC proteins, are useful for inhibiting the growth of a tumour, tumour
XX CC metastasis and/or angiogenesis, and including disorders such as ischaemic
XX CC heart disease, peripheral vascular disease, wound healing, bone repair,
XX CC rheumatoid arthritis and diabetic retinopathy. The present sequence is
XX CC used in the exemplification of the present invention.
XX SQ Sequence 489 AA;
Query Match 55.3%; Score 1241; DB 7; Length 489;
Best Local Similarity 85.5%; Pred. No. 1.1e-73;
```

```
Matches 236; Conservative 4; Mismatches 14; Indels 22; Gaps 2;
QY 2 DKHTCTCPCPAPBELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 1 DKHTCTCPCPAPBELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60
QY 62 GVEVHNNAKTPREOVNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 61 GVEVHNNAKTPREOVNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
Db 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
QY 182 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTKQSLSPK----- 228
Db 181 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTKQSLSPKGGGGGGGGGIQRD 240
QY 229 -----ETFPKYLHYDEETSHQLLCKCPPTGYLKHQCTAKWKTCAPCPDHYHYTSMHTSDECLY 289
Db 241 PGYPRDLMPPP-----DLATSPKSPFKIPPTFINE 272

RESULT 15
AAB17951
ID AAB17951 standard; protein; 248 AA.
XX AC AAB17951;
XX DT 31-OCT-2000 (first entry)
XX DE Fc-TNF-alpha inhibitor fusion protein sequence SEQ ID NO:1056.
XX KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
XX KW autoimmune disease; cytostatic; antiaesthetic; thrombolytic; VEGF;
XX KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
XX KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
XX KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
XX KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
XX KW thrombosis; pharmaceutical.
XX OS Synthetic.
XX PN WO2000024782-A2.
XX PD 04-MAY-2000.
XX PF 25-OCT-1999; 99WO-US025044.
XX PR 23-OCT-1998; 98US-0105371P.
XX PR 22-OCT-1999; 99US-00428082.
XX PA (AMGE-) AMGEN INC.
XX PI Feige U, Liu C, Cheatham J, Boone TC;
XX WPI; 2000-350702/30.
XX DR N-PSDB; AAA69501.
XX PT Novel composition of matter comprising an Fc domain and pharmacologically
XX PT active peptides, useful for treating cancer and autoimmune diseases.
XX PS Example 4; Page 568-569; 608pp; English.
XX CC The present invention describes composition of matter (I) comprising an
XX CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
XX CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
XX CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
XX CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P3-(L4)f-P4 where P1, P2,
XX CC P3, and P4 = are each independently sequences of pharmacologically active
XX CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
XX CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
XX CC of a and b is 1. The composition can have cytostatic, antiaesthetic,
```

CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAG69443 to AAG69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 248 AA;

Query Match 55.2%; Score 1240; DB 3; Length 248;
Best Local Similarity 95.1%; Pred. No. 5.7e-74;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Qy 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120
Db 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120
Qy 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
Db 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYTQKSLSLSPGKGGGGDLPHYK 240
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYTQKSLSLSPGKGGGGDLPHYK 240
Qy 241 ETS 243
Db 241 NTS 243

Search completed: March 8, 2005, 14:38:22
Job time : 87.1064 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:28:42 ; Search time 21.9235 Seconds
(without alignments)
1365.399 Million cell updates/sec

Title: US-09-389-782A-8
Perfect score: 2246
Sequence: 1 MDKTHCPCPAPELLGGPS.....QKGNATHNDCGNSESTOK 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1240	55.2	248	4	US-09-428-082B-1056
2	1238	55.1	228	4	US-09-428-082B-2
3	1238	55.1	228	4	US-09-847-249A-2
4	1238	55.1	228	4	US-09-840-669B-2
5	1238	55.1	228	4	US-09-843-221A-2
6	1238	55.1	228	4	US-09-709-704A-2
7	1238	55.1	228	4	US-09-422-838C-5
8	1238	55.1	243	4	US-09-428-082B-1068
9	1238	55.1	247	4	US-09-428-082B-6
10	1238	55.1	248	4	US-09-428-082B-1060
11	1238	55.1	252	4	US-09-428-082B-1064
12	1238	55.1	253	4	US-09-428-082B-16
13	1238	55.1	268	4	US-09-428-082B-8
14	1238	55.1	269	4	US-09-422-838C-46
15	1238	55.1	277	4	US-09-428-082B-22
16	1237	55.1	389	3	US-09-131-247-14
17	1237	55.1	389	4	US-09-784-623-14
18	1234	54.9	229	4	US-09-122-144-2
19	1234	54.9	347	1	US-07-940-861-43
20	1234	54.9	347	1	US-08-459-512-43
21	1234	54.9	347	2	US-08-459-657-43
22	1234	54.9	347	2	US-08-460-132-43
23	1234	54.9	347	3	US-08-466-465-8
24	1234	54.9	347	4	US-09-730-465-8
25	1234	54.9	347	5	PCT-US92-02050-43
26	1234	54.9	399	4	US-09-832-659A-2
27	1234	54.9	418	4	US-09-832-659A-42

28	1234	54.9	423	4	US-09-832-659A-44	Sequence 44, Appl
29	1234	54.9	446	4	US-09-157-452B-12	Sequence 12, Appl
30	1234	54.9	482	3	US-09-189-129-2	Sequence 2, Appl
31	1234	54.9	482	4	US-09-824-286-2	Sequence 2, Appl
32	1233.5	54.9	394	4	US-09-854-864-31	Sequence 31, Appl
33	1233	54.9	232	2	US-08-595-043A-50	Sequence 50, Appl
34	1233	54.9	232	4	US-09-968-362A-26	Sequence 26, Appl
35	1233	54.9	235	3	US-09-131-247-6	Sequence 6, Appl
36	1233	54.9	235	4	US-09-784-623-6	Sequence 6, Appl
37	1233	54.9	247	4	US-09-428-082B-12	Sequence 12, Appl
38	1233	54.9	248	4	US-09-428-082B-1058	Sequence 1058, Ap
39	1233	54.9	248	4	US-09-428-082B-1062	Sequence 1062, Ap
40	1233	54.9	250	4	US-09-428-082B-1070	Sequence 1070, Ap
41	1233	54.9	252	4	US-09-428-082B-1066	Sequence 1066, Ap
42	1233	54.9	253	4	US-09-428-082B-18	Sequence 18, Appl
43	1233	54.9	269	4	US-09-428-082B-10	Sequence 10, Appl
44	1233	54.9	277	4	US-09-428-082B-20	Sequence 20, Appl
45	1233	54.9	281	4	US-09-854-864-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-428-082B-1056
; Sequence 1056, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPHA INHIBITORS
US-09-428-082B-1056

Query Match	55.2%	Score	1240;	DB	4;	Length	248;
Best Local Similarity	95.1%	Pred. No.	2.2e-98;				
Matches	231;	Conservative	3;	Mismatches	9;	Indels	0;
Gaps	0;						
Qy	1	MDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV	60				
Db	1	MDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV	60				
Qy	61	DGVEVHNAKTKPREQYNSYTYRVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKA	120				
Db	61	DGVEVHNAKTKPREQYNSYTYRVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKA	120				
Qy	121	KQPREPQYVITPPSRDELTKNQVSLTCLVKGFYPSDIAVEVNESGNQPENNYKTTTPVLD	180				
Db	121	KQPREPQYVITPPSRDELTKNQVSLTCLVKGFYPSDIAVEVNESGNQPENNYKTTTPVLD	180				
Qy	181	SGSFLYSLKLTVDKSRWQQGVFSCSVNHEALHHYTKSLSPGKTFPPKYLHYDE	240				
Db	181	SGSFLYSLKLTVDKSRWQQGVFSCSVNHEALHHYTKSLSPGKTFPPKYLHYDE	240				
Qy	241	ETS 243					
Db	241	NTS 243					

RESULT 2
US-09-428-082B-2
; Sequence 2, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: HUMAN
US-09-428-082B-2

Query Match 55.1%; Score 1238; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.9e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
QY 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 3
US-09-847-249A-2
; Sequence 2, Application US/09847249A
; Patent No. 6677136
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE
; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-249A-2

Query Match 55.1%; Score 1238; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.9e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

QY 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 4
US-09-840-669B-2
; Sequence 2, Application US/09840669B
; Patent No. 6743778
; GENERAL INFORMATION:
; APPLICANT: KOHNO, TADAHIKO
; TITLE OF INVENTION: APO-AI/AII PEPTIDE DERIVATIVES
; FILE REFERENCE: A-690
; CURRENT APPLICATION NUMBER: US/09/840,669B
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/198,920
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-669B-2

Query Match 55.1%; Score 1238; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.9e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
QY 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 5
US-09-843-221A-2
; Sequence 2, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27

```

; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-2

Query Match          55.1%; Score 1238; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.9e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

QY 61 DGEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISK 120
DB 61 DGEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISK 120

QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 6
US-09-709-704A-2
; Sequence 2, Application US/09709704A
; Patent No. 6808902
; GENERAL INFORMATION:
; APPLICANT: TREUHEIT, MICHAEL J.
; APPLICANT: O'CONNER, SHEILA R.
; APPLICANT: KOSKY, ANDREW A.
; TITLE OF INVENTION: PROCESS FOR CORRECTION OF A DISULFIDE MISFOLD IN FC MOLECULES
; FILE REFERENCE: A-584
; CURRENT APPLICATION NUMBER: US/09/709,704A
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/165,188
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-709-704A-2

Query Match          55.1%; Score 1238; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.9e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

QY 61 DGEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISK 120
DB 61 DGEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISK 120

QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 7
```

```

US-09-422-838C-5
; Sequence 5, Application US/09422838C
; Patent No. 6835809
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET C.
; TITLE OF INVENTION: Thrombopoietic Compounds
; FILE REFERENCE: 01017/36283
; CURRENT APPLICATION NUMBER: US/09/422,838C
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,348
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 5
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-422-838C-5

Query Match          55.1%; Score 1238; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.9e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

QY 61 DGEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISK 120
DB 61 DGEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISK 120

QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 8
US-09-428-082B-1068
; Sequence 1068, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1068
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC MMP INHIBITOR
US-09-428-082B-1068

Query Match          55.1%; Score 1238; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.2e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 MDKTHCTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHCTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 9

US-09-428-082B-6
; Sequence 6, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-TMP
US-09-428-082B-6

Query Match 55.1%; Score 1238; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.3e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHCTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHCTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 10

US-09-428-082B-1060
; Sequence 1060, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1060
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-IL-1 ANTAGONIST
US-09-428-082B-1060

Query Match 55.1%; Score 1238; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.3e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHCTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHCTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 11

US-09-428-082B-1064
; Sequence 1064, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1064
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-VEGF ANTAGONIST
US-09-428-082B-1064

Query Match 55.1%; Score 1238; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.3e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHCTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHCTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 12

US-09-428-082B-16
; Sequence 16, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428, 082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-BMP
US-09-428-082B-16

Query Match 55.1%; Score 1238; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.4e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120
DB 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 13

US-09-428-082B-8
; Sequence 8, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428, 082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8

; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-TMP-TMP
US-09-428-082B-8

Query Match 55.1%; Score 1238; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 3.6e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120
DB 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 14

US-09-422-838C-46
; Sequence 46, Application US/09422838C
; Patent No. 6835809
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET C.
; TITLE OF INVENTION: Thrombopoietic Compounds
; FILE REFERENCE: 01017/36263
; CURRENT APPLICATION NUMBER: US/09/422,838C
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,348
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 46
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-422-838C-46

Query Match 55.1%; Score 1238; DB 4; Length 269;
Best Local Similarity 100.0%; Pred. No. 3.7e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120
DB 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 15

US-09-428-082B-22
; Sequence 22, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-EMP-EMP
US-09-428-082B-22

Query Match 55.1%; Score 1238; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKA 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLD 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTOKSLSLSPGK 228
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTOKSLSLSPGK 228

Search completed: March 8, 2005, 14:48:15
Job time : 22.9235 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:44:50 ; Search time 60.5885 Seconds
(without alignments)
2177.757 Million cell updates/sec

Title: US-09-389-782A-8

Perfect score: 2246

Sequence: 1 MDKTHTCPAPPELLGGPS.....QKGNATHDNCISGSESTOK 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 32904822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2246	100.0	401	10	US-09-389-782-8
2	1271.5	56.6	861	15	US-10-449-548-52
3	1271.5	56.6	861	15	US-10-403-676-52
4	1271.5	56.6	878	15	US-10-449-548-54
5	1271.5	56.6	878	15	US-10-403-676-54
6	1249	55.6	731	9	US-09-825-012-46
7	1249	55.6	741	9	US-09-825-012-55
8	1241	55.3	489	15	US-10-385-802-44
9	1240	55.2	248	15	US-10-609-217-1056
10	1240	55.2	248	15	US-10-632-388-1056
11	1240	55.2	248	15	US-10-651-723-1056
12	1240	55.2	248	15	US-10-645-761-1056
13	1240	55.2	248	15	US-10-666-696-1056

14	1240	55.2	248	15	US-10-653-048-1056	Sequence 1056, Ap
15	1238	55.1	228	9	US-09-847-712-2	Sequence 2, Appli
16	1238	55.1	228	9	US-09-847-712-2	Sequence 2, Appli
17	1238	55.1	228	10	US-09-847-249A-2	Sequence 2, Appli
18	1238	55.1	228	10	US-09-843-221A-2	Sequence 2, Appli
19	1238	55.1	228	10	US-09-840-669B-2	Sequence 2, Appli
20	1238	55.1	228	14	US-10-269-806-32	Sequence 32, Appli
21	1238	55.1	228	14	US-10-145-206-2	Sequence 2, Appli
22	1238	55.1	228	15	US-10-609-217-2	Sequence 2, Appli
23	1238	55.1	228	15	US-10-632-388-2	Sequence 2, Appli
24	1238	55.1	228	15	US-10-651-723-2	Sequence 2, Appli
25	1238	55.1	228	15	US-10-645-761-2	Sequence 2, Appli
26	1238	55.1	228	15	US-10-666-696-2	Sequence 2, Appli
27	1238	55.1	228	15	US-10-653-048-2	Sequence 2, Appli
28	1238	55.1	228	15	US-10-666-480-60	Sequence 60, Appli
29	1238	55.1	228	17	US-10-925-183-2	Sequence 2, Appli
30	1238	55.1	243	14	US-10-269-806-152	Sequence 152, App
31	1238	55.1	243	15	US-10-609-217-1068	Sequence 1068, Ap
32	1238	55.1	243	15	US-10-632-388-1068	Sequence 1068, Ap
33	1238	55.1	243	15	US-10-651-723-1068	Sequence 1068, Ap
34	1238	55.1	243	15	US-10-645-761-1068	Sequence 1068, Ap
35	1238	55.1	243	15	US-10-666-696-1068	Sequence 1068, Ap
36	1238	55.1	243	15	US-10-653-048-1068	Sequence 1068, Ap
37	1238	55.1	247	15	US-10-609-217-6	Sequence 6, Appli
38	1238	55.1	247	15	US-10-632-388-6	Sequence 6, Appli
39	1238	55.1	247	15	US-10-651-723-6	Sequence 6, Appli
40	1238	55.1	247	15	US-10-645-761-6	Sequence 6, Appli
41	1238	55.1	247	15	US-10-666-696-6	Sequence 6, Appli
42	1238	55.1	247	15	US-10-653-048-6	Sequence 6, Appli
43	1238	55.1	248	15	US-10-609-217-1060	Sequence 1060, Ap
44	1238	55.1	248	15	US-10-632-388-1060	Sequence 1060, Ap
45	1238	55.1	248	15	US-10-651-723-1060	Sequence 1060, Ap

ALIGNMENTS

RESULT 1
US-09-389-782-8
; Sequence 8, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 401
; TYPE: PPT
; ORGANISM: Human
US-09-389-782-8

Query Match 100.0%; Score 2246; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.4e-145;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV	60
Db	1	MDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV	60
QY	61	DGVEVHNATKEREQYNSYTYVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKA	120
Db	61	DGVEVHNATKEREQYNSYTYVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKA	120
QY	121	KGQPREQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	180
Db	121	KGQPREQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	180

QY 191 SDGSFFLYSKLTVDKSRWQGNVSCSVMHREALNHNHYTKSLSLSPGKETFPFKYLHYDE 240
 Db 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMHREALNHNHYTKSLSLSPGKETFPFKYLHYDE 240
 QY 241 ETSHQLLCDKCPGTYLKQHTAKWTVCAPCPDHYTDSWHTSDECLYSPVKELQYV 300
 Db 241 ETSHQLLCDKCPGTYLKQHTAKWTVCAPCPDHYTDSWHTSDECLYSPVKELQYV 300
 QY 301 KOENRTHNRVCECKEGRYLEIEFCLKXRSPPGFGVVQAGTPERNTVCKRCPDGPFNS 360
 Db 301 KOENRTHNRVCECKEGRYLEIEFCLKXRSPPGFGVVQAGTPERNTVCKRCPDGPFNS 360
 QY 361 TSSKAPCKKTNCSVFGLLLTQGNATHDNCNSESSTQK 401
 Db 361 TSSKAPCKKTNCSVFGLLLTQGNATHDNCNSESSTQK 401

RESULT 2

US-10-449-548-52
 ; Sequence 52, Application US/10449548
 ; Publication No. US20040018977A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alvarez, Enrique
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Dhanabal, Mohanraj
 ; APPLICANT: Kramcov, Nikolai V.
 ; APPLICANT: LaRoche, William J.
 ; APPLICANT: Li, Li
 ; APPLICANT: Lichenstein, Henri
 ; APPLICANT: Ooi, Chean Eng
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Zhong, Mei
 ; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
 ; FILE REFERENCE: 15966-540CIP2
 ; CURRENT APPLICATION NUMBER: US/10/449,548
 ; CURRENT FILING DATE: 2003-05-30
 ; PRIOR APPLICATION NUMBER: 09/520,781
 ; PRIOR FILING DATE: 2000-03-03
 ; PRIOR APPLICATION NUMBER: 60/123,667
 ; PRIOR FILING DATE: 1999-03-09
 ; PRIOR APPLICATION NUMBER: 60/234,082
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: 60/233,798
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 60/174,485
 ; PRIOR FILING DATE: 2000-01-04
 ; PRIOR APPLICATION NUMBER: 10/403,676
 ; PRIOR FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: 60/371,002
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/384,798
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: 60/402,407
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 60/443,062
 ; PRIOR FILING DATE: 2003-01-28
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: CuroSeqList version 0.1
 ; SEQ ID NO 52
 ; LENGTH: 861
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-449-548-52

Query Match 56.6%; Score 1271.5; DB 15; Length 861;
 Best Local Similarity 63.8%; Pred. No. 2.4e-78;
 Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;
 QY 2 DKHTCCPCAPPELLGGSPVFLPPPKDQTLMSITPEVTCVVVDVSHEDPEVKFNWYVD 61
 Db 1 DKHTCCPCAPPELLGGSPVFLPPPKDQTLMSITPEVTCVVVDVSHEDPEVKFNWYVD 60

QY 62 GVEVHNKTPREQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
 Db 61 GVEVHNKTPREQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120
 QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
 Db 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
 QY 182 DGSFFLYSKLTVDKSRWQGNVSCSVMHREALNHNHYTKSLSLSPGK 234
 Db 181 DGSFFLYSKLTVDKSRWQGNVSCSVMHREALNHNHYTKSLSLSPGKGGGGGGGFP 239
 QY 235 YLHYDEE---TSHQLLCKDKCPGTYLKQHTAKWTVCAPCPDHYTDSWHTSDECLYSPVKELQYV 269
 Db 240 ---DSEPIISISH-----GNTKQYVPVGVGHKPGRTTQRRHLDIQIMIMINWGLY 286
 QY 270 APCPDHYT---DSWHTSDECLYSPVKELQYVQECNRTNRYCECK-EGRYLE---- 321
 Db 287 TAARDHIYTVDTIDTSHTEE--IYCS---KLTWKSROAD---VDTCRMKGKHKDECHN 336
 QY 322 -IEFCLKXRSPPGFGVVQAGTPERNTVCKRC-----PDGFFSNETSSKAPC---RKHT 371
 Db 337 FIKVLLKND---DALFVCGTNAFNPSCRNYKMDTLEP---FGDEFSGMARCPCYDAKHA 389
 QY 372 NCSVF 376
 Db 390 NVALF 394

RESULT 3

US-10-403-676-52
 ; Sequence 52, Application US/10403676
 ; Publication No. US20040029150A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsobrook II, John
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Gerlach, Valerie L.
 ; APPLICANT: Groese, William M.
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: LaRoche, William J.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Li, Li
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Peyman, John A.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Reiger, Daniel
 ; APPLICANT: Rothenberg, Mark E.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Taupier, Raymond J.
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Zerhusen, Bryan D.
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
 ; FILE REFERENCE: 21402-573B
 ; CURRENT APPLICATION NUMBER: US/10/403,676
 ; CURRENT FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: 60/123,667
 ; PRIOR FILING DATE: 1999-03-09
 ; PRIOR APPLICATION NUMBER: 09/520,781
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 09/957,187
 ; PRIOR FILING DATE: 2001-09-19

```

; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 52
; LENGTH: 861
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-52

Query Match          56.6%; Score 1271.5; DB 15; Length 861;
Best Local Similarity 63.8%; Pred. No. 2.4e-78;
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

QY 2 DKHTCTPPCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 1 DKHTCTPPCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60

QY 62 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 61 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLD 181
DB 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLD 180

QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK-----ETFPK 234
DB 181 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGFP 239

QY 235 YLHYDEE---TSHQLLCKDCPPGTYLKQH-----CTAKWK-----TVC 269
DB 240 ----DSEPTISISH-----GNVTQYPVFVGHKPGRNTTQHRHLDIQIMINMGTL 286

QY 270 APCPDHYIT---DSWHTSDECLYCSVPCKELQVVKQECNTHNRVCECK-EGRYL 321
DB 287 IAARDHIYTVDTIDTSHTEE--IYCS---KKLTWKSROAD-----VDTCRMKGKHKDECHN 336

QY 322 -IEFCLKHSRCPGFGVQAGTPERNVTCKRC-----PDGFFSNETSAPK- --RKHT 371
DB 337 FIKVLLKKND----DALFVCGTNAFPNFCRNYKMDTLEP---FGDFSGMARCPCYDAKHA 389

QY 372 NCSVF 376
DB 390 NVALF 394

RESULT 4
US-10-449-548-54
; Sequence 54, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRoche, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng

```

```

; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 54
; LENGTH: 878
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-54

```

```

Query Match          56.6%; Score 1271.5; DB 15; Length 878;
Best Local Similarity 63.8%; Pred. No. 2.4e-78;
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

QY 2 DKHTCTPPCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 1 DKHTCTPPCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60

QY 62 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 61 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLD 181
DB 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLD 180

QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK-----ETFPK 234
DB 181 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGFP 239

QY 235 YLHYDEE---TSHQLLCKDCPPGTYLKQH-----CTAKWK-----TVC 269
DB 240 ----DSEPTISISH-----GNVTQYPVFVGHKPGRNTTQHRHLDIQIMINMGTL 286

QY 270 APCPDHYIT---DSWHTSDECLYCSVPCKELQVVKQECNTHNRVCECK-EGRYL 321
DB 287 IAARDHIYTVDTIDTSHTEE--IYCS---KKLTWKSROAD-----VDTCRMKGKHKDECHN 336

QY 322 -IEFCLKHSRCPGFGVQAGTPERNVTCKRC-----PDGFFSNETSAPK- --RKHT 371
DB 337 FIKVLLKKND----DALFVCGTNAFPNFCRNYKMDTLEP---FGDFSGMARCPCYDAKHA 389

QY 372 NCSVF 376
DB 390 NVALF 394

```

RESULT 5


```
QY 242 TSHQLLCKCPGTYLKQ-----HCTAKWK---TVCACPDHYH-1----- 277
Db 481 TGETKMSNATLVSVIVQILSRDYIALVOEVRDLSHTAVGKLLDNLNQDAPDTYHYVWSE 540
QY 278 -----TDSWHTSDECLYCSVPVKELQYVQECNRTNHRVCECK 315
Db 541 PLGRNSYKERYLVYRPPQVSAVDSYYDDGCEPCG-----NDTFNREPAIV 587
QY 316 E--GRYLEI-EFCLKXRSPPGFGVVQ 339
Db 588 RFFSRFTEVREPAIVPLHAAPGDAVAE 614

RESULT 7
US-09-825-012-55
; Sequence 55, Application US/09825012
; Patent No. US2002012798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 741
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMEG1 heavy chain - DNase I fusion
US-09-825-012-55

Query Match 55.6%; Score 1249; DB 9; Length 741;
Best Local Similarity 65.6%; Pred. No. 6.9e-77;
Matches 254; Conservative 15; Mismatches 56; Indels 62; Gaps 6;

QY 2 DKHTCCPPCAPPELLGGPSVFLFPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 241 DKHTCCPPCAPPELLGGPSVFLFPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVD 300
QY 62 GVEVHNATKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAK 121
Db 301 GVEVHNATKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAK 360
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLD 181
Db 361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLD 420
QY 182 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPGKTTTPVLD 241
Db 421 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPGKTTTPVLD 480
QY 242 TSHQLLCKCPGTYLKQ-----HCTAKWK---TVCACPDHYH-1----- 277
Db 481 TGETKMSNATLVSVIVQILSRDYIALVOEVRDLSHTAVGKLLDNLNQDAPDTYHYVWSE 540
QY 278 -----TDSWHTSDECLYCSVPVKELQYVQECNRTNHRVCECK 315
Db 541 PLGRNSYKERYLVYRPPQVSAVDSYYDDGCEPCG-----NDTFNREPAIV 587
QY 316 E--GRYLEI-EFCLKXRSPPGFGVVQ 339
Db 588 RFFSRFTEVREPAIVPLHAAPGDAVAE 614
```

RESULT 8
US-10-385-802-44

```
; Sequence 44, Application US/10385802
; Publication No. US20030224991A1
; GENERAL INFORMATION:
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: LaRoche, William J.
; APPLICANT: Lichenstein, Henri
; APPLICANT: Wu, Frank
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND AMINO ACID SEQUENCES OF
; FILE REFERENCE: 15966-517UB
; CURRENT APPLICATION NUMBER: US/10/385,802
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/363,266
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 44
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-385-802-44

Query Match 55.3%; Score 1241; DB 15; Length 489;
Best Local Similarity 85.5%; Pred. No. 1.5e-76;
Matches 236; Conservative 4; Mismatches 14; Indels 22; Gaps 2;

QY 2 DKHTCCPPCAPPELLGGPSVFLFPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 1 DKHTCCPPCAPPELLGGPSVFLFPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVD 60
QY 62 GVEVHNATKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAK 121
Db 61 GVEVHNATKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAK 120
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLD 181
Db 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLD 180
QY 182 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPGKTTTPVLD 228
Db 181 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPGKTTTPVLD 240
QY 229 -----ETPPKYLHYDETSHTQLLCKCPGTYLKQ 259
Db 241 PGYPRDLMPPP-----DLATSPKSPFKIPPVTFINE 272

RESULT 9
US-10-609-217-1056
; Sequence 1056, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: PEIGE, ULRICH
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPHA INHIBITORS
US-10-609-217-1056
```

```
Query Match      55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKSLSPGKETPPPKYLHYDE 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKSLSPGKETPPPKYLHYDE 240
QY 241 ETS 243
DB 241 NTS 243

RESULT 10
US-10-632-388-1056
; Sequence 1056, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; PRIOR FILING DATE: 2003-07-31
; PRIOR FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNP-ALPA INHIBITORS
US-10-632-388-1056

Query Match      55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKSLSPGKETPPPKYLHYDE 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKSLSPGKETPPPKYLHYDE 240
QY 241 ETS 243
DB 241 NTS 243

RESULT 11
US-10-651-723-1056
; Sequence 1056, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; PRIOR FILING DATE: 2003-08-29
; PRIOR FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNP-ALPA INHIBITORS
US-10-651-723-1056

Query Match      55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKSLSPGKETPPPKYLHYDE 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKSLSPGKETPPPKYLHYDE 240
QY 241 ETS 243
DB 241 NTS 243

RESULT 12
US-10-645-761-1056
; Sequence 1056, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; PRIOR FILING DATE: 2003-08-18
; PRIOR FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNP-ALPA INHIBITORS
US-10-632-388-1056

Query Match      55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKSLSPGKETPPPKYLHYDE 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKSLSPGKETPPPKYLHYDE 240
QY 241 ETS 243
DB 241 NTS 243
```

```
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPHA INHIBITORS
US-10-645-761-1056

Query Match          55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

QY 181 SDGSFPLYSKLTVDKSRWQQGNVFCSVVMHEALHNNHYTKQSLSPGKGTFFPPKYLHYDE 240
DB 181 SDGSFPLYSKLTVDKSRWQQGNVFCSVVMHEALHNNHYTKQSLSPGKGTFFPPKYLHYDE 240

QY 241 ETS 243
DB 241 NTS 243

RESULT 13
US-10-666-696-1056
; Sequence 1056, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPHA INHIBITORS
US-10-666-696-1056

Query Match          55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

QY 181 SDGSFPLYSKLTVDKSRWQQGNVFCSVVMHEALHNNHYTKQSLSPGKGTFFPPKYLHYDE 240
DB 181 SDGSFPLYSKLTVDKSRWQQGNVFCSVVMHEALHNNHYTKQSLSPGKGTFFPPKYLHYDE 240

QY 241 ETS 243
DB 241 NTS 243

RESULT 14
US-10-653-048-1056
; Sequence 1056, Application US/10653048
; Publication No. US2004008778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPHA INHIBITORS
US-10-653-048-1056

Query Match          55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

QY 181 SDGSFPLYSKLTVDKSRWQQGNVFCSVVMHEALHNNHYTKQSLSPGKGTFFPPKYLHYDE 240
DB 181 SDGSFPLYSKLTVDKSRWQQGNVFCSVVMHEALHNNHYTKQSLSPGKGTFFPPKYLHYDE 240

QY 241 ETS 243
DB 241 NTS 243

RESULT 15
US-09-847-712-2
; Sequence 2, Application US/09847712
```

; Patent No. US20020090646A1
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: REYNOLDS, ANGELA
; TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
; FILE REFERENCE: A-684
; CURRENT APPLICATION NUMBER: US/09/847,712
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,511
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-712-2

Query Match 55.1%; Score 1238; DB 9; Length 228;
Best Local Similarity 100.0%; Pred. No. 1e-76;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKHTCPCPAPELGGPSVFLPPKPKDTLMISPTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKHTCPCPAPELGGPSVFLPPKPKDTLMISPTPEVTCVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNATKPREQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNATKPREQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCFVSNVHEALHNHYTOKLSLSFGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCFVSNVHEALHNHYTOKLSLSFGK 228

Search completed: March 8, 2005, 15:16:17
Job time : 61.5885 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:20:42 ; Search time 16.3429 Seconds
(without alignments)
2360.831 Million cell updates/sec

Title: US-09-389-782A-8
Perfect score: 2246
Sequence: 1 MKTHTCPPCPAPPELLGGPS.....QKGNATHDNCISGSESTOK 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 791.*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1233	54.9	255	4	Ig gamma-1 chain C
2	1233	54.9	330	1	Ig gamma-1 chain C
3	1227	54.6	374	2	Ig heavy chain V r
4	1180	52.5	234	2	Ig gamma chain C r
5	1146	51.0	377	2	Ig gamma-3 chain C
6	1144	50.9	377	2	Ig gamma-3 chain C
7	1142.5	50.9	326	1	Ig gamma-2 chain C
8	1135	50.5	327	1	Ig gamma-4 chain C
9	1121	49.9	289	1	Ig gamma-3 heavy c
10	918.5	40.9	323	1	Ig gamma chain C r
11	906.5	40.4	328	2	Ig gamma 2b chain
12	906.5	40.4	328	2	Ig gamma 2a chain
13	903.5	40.2	277	2	Ig gamma 4 chain C
14	889	39.6	329	1	Ig gamma-2 chain C
15	885.5	39.4	328	2	Ig gamma 1 chain c
16	878.5	39.1	328	2	Ig gamma 3 chain c
17	855.5	38.1	470	2	Ig heavy chain pre
18	846	37.7	308	2	Ig heavy chain C r
19	846	37.7	472	2	Ig gamma-1 chain -
20	845.5	37.6	329	1	Ig gamma-3 chain C
21	838	37.3	333	2	Ig gamma-2b chain
22	835.5	37.2	398	1	Ig gamma-3 chain C
23	827.5	36.8	444	2	monoclonal antibod
24	818.5	36.4	326	2	Ig gamma-1 chain C
25	817.5	36.4	324	1	Ig gamma-1 chain C
26	812.5	36.2	393	1	Ig gamma-1 chain C
27	809.5	36.0	329	2	Ig gamma-2c chain
28	809	36.0	330	1	Ig gamma-2a chain
29	809	36.0	469	2	Ig gamma-2a chain

30	804	35.8	399	1	G2MSAM	Ig gamma-2a chain
31	802	35.7	335	1	G2MSAB	Ig gamma-2a chain
32	794	35.4	446	2	S40295	Ig gamma-2a chain
33	785.5	35.0	322	2	PS0019	Ig gamma-2a chain
34	779	34.7	474	1	G2MS11	Ig gamma-2b chain
35	774	34.5	405	1	G2MSBM	Ig gamma-2b chain
36	764	34.0	327	2	S06611	Ig gamma-2 chain C
37	757	33.7	475	2	S01321	Ig gamma-2b chain
38	707	31.5	180	2	I46732	Ig gamma heavy cha
39	577.5	25.7	249	2	S69340	Ig heavy chain VHI
40	574.5	25.6	218	2	A36040	Ig heavy chain V-I
41	571	25.4	152	2	S14236	Ig gamma-1 chain C
42	395.5	17.6	572	2	B46529	Ig Y heavy chain (
43	362	16.1	343	2	S25644	Ig mu chain C regi
44	362	16.1	453	2	S37768	Ig mu chain C regi
45	361	16.1	455	1	MHMS	Ig mu chain C regi

ALIGNMENTS

RESULT 1

S31866
Ig gamma-1 chain C region - synthetic
C/Species: synthetic
A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C/Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C/Accession: S31866
R/Filpula, D.
submitted to the EMBL Data Library, February 1993
A/Description: Screening method for protein-protein interactions of cloned gene products.
A/Reference number: S31866
A/Accession: S31866
A/Molecule type: mRNA
A/Residues: 1-255 <PIL>
A/Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C/Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match	54.9%;	Score	1233;	DB	4;	Length	255;
Best Local Similarity	100.0%;	Pred. No.	4.2e-71;				
Matches	227;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	2	DKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	61				
Db	29	DKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	88				
QY	62	GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	121				
Db	89	GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	148				
QY	122	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	181				
Db	149	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	208				
QY	182	DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK	228				
Db	209	DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK	255				

RESULT 2

GHU
Ig gamma-1 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C/Accession: A93433; S36861; S3887; B90563; A90564; B91668; A91723; A02146
R/Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.
A/Reference number: A93433; MUID:82274238; PMID:6287432
A/Accession: A93433
A/Molecule type: DNA

A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the GIm(17) allotypic marker, 97-Lys, and the GIm(1) markers,
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obara, M.; Nakai, S.; Honjo, T.
Call 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113,235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Maxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the GIm(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Note: this sequence has the GIm(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the GIm(17) and GIm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOI; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the GIm(3) and GIm(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
endamide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1, 114/1, 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 54.9%; Score 1233; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.5e-71;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCCPCPAPELLGGPSVFLPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
|||||
Db 104 DKHTCCPCPAPELLGGPSVFLPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 163

QY 62 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
|||||
Db 164 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 181
|||||
Db 224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 283

QY 182 DGSFPLYSKLTVDKSRWQQGNVFCSSVNHAEALHNHYTQKSLSLSPGK 228
|||||
Db 284 DGSFPLYSKLTVDKSRWQQGNVFCSSVNHAEALHNHYTQKSLSLSPGK 330

RESULT 3

S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogné, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 54.68%; Score 1227; DB 2; Length 374;
Best Local Similarity 99.1%; Pred. No. 1.5e-70;
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCCPCPAPELLGGPSVFLPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
|||||
Db 148 DKHTCCPCPAPELLGGPSVFLPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 207

QY 62 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
|||||
Db 208 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 181
|||||
Db 268 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 327

```
QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSPGK 228
Db 328 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSPGK 374

RESULT 4
PT0207
Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 <EHR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 52.5%; Score 1180; DB 2; Length 234;
Best Local Similarity 98.6%; Pred. No. 8.5e-68;
Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 15 DTHHTCPPCAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 74

QY 62 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 75 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 134

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
Db 135 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 194

QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSPGK 228
Db 195 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSPGK 234

RESULT 5
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056
C;Genetics:
A;Gene: IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 51.0%; Score 1146; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 2e-65;
Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 151 DTPPCPCRCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 210

RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.9%; Score 1144; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 2.7e-65;
Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 151 DTPPCPCRCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 210

QY 62 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 211 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 270

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
Db 271 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 330

QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSPGK 228
Db 331 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSPGK 377

RESULT 7
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; PJ
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
```

```
QY 62 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 211 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 270

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
Db 271 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 330

QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSPGK 228
Db 331 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSPGK 377

RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.9%; Score 1144; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 2.7e-65;
Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 151 DTPPCPCRCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 210

QY 62 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 211 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 270

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
Db 271 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 330

QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSPGK 228
Db 331 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSPGK 377

RESULT 7
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; PJ
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
```


A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24,'E',26-57,'EV',60-85,'132-171','ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin S
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to The Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69054124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.9%; Score 1142.5; DB 1; Length 326;
Best Local Similarity 94.1%; Pred. No. 2.9e-65;
Matches 209; Conservative 8; Mismatches 4; Indels 1; Gaps 1;
QY 7 CPPCPAPPELLGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
DB 106 CPPCPAPP-VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH 164
QY 67 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
DB 165 NAKTKPREQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPRE 224
QY 127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 186
DB 225 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 284
QY 187 LYSKLTVDKSRWQQGNVSCVMHRLNHYTQKSLSPGK 228
DB 285 LYSKLTVDKSRWQQGNVSCVMHRLNHYTQKSLSPGK 326

RESULT 8

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004

C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A:Cross-references: UNIPROT:P01861

A:Note: The sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant re

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30;81-326 <PIN>

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1, 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,141-201,247-305/Disulfide bonds: #status predicted

F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.5%; Score 1135; DB 1; Length 327;
Best Local Similarity 93.7%; Pred. No. 8.6e-65;
Matches 208; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 7 CPPCPAPPELLGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66

DB 106 CPPCPAPPELLGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 165

QY 67 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126

DB 166 NAKTKPREQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPRE 225

QY 127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 186

DB 226 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 285

QY 187 LYSKLTVDKSRWQQGNVSCVMHRLNHYTQKSLSPGK 228

DB 286 LYSKLTVDKSRWQQGNVSCVMHRLNHYTQKSLSPGK 327

RESULT 9

G3HUMI

Ig gamma-3 heavy chain disease proteins - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1979 #sequence revision 23-Oct-1981 #text_change 16-Jul-1999

C:Accession: A90442; A92219; A90198; A93915; A02149

R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.

Biochemistry 19, 4304-4308, 1980

A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-

A:Reference number: A90442; MUID:81021548; PMID:6774747

A:Contents: heavy chain disease protein Wis
 A:Accession: A90442
 A:Molecule type: protein
 A:Residues: 1-289 <PRA>
 A>Note: this molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
 A>Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co
 A>Note: the sequence of residues 42-76 was taken from the reference that follows
 R:Michaelson, T.E.; Frangione, B.; Franklin, E.C.
 J. Biol. Chem. 252, 883-889, 1977
 A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
 A:Reference number: A92219; MUID:77118561; PMID:402363
 A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
 A:Accession: A92219
 A:Molecule type: protein
 A:Residues: 12-97 <MIC>
 A>Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
 A:Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
 A:Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter
 R:Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
 Biochem. Biophys. Res. Commun. 71, 907-914, 1976
 A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
 A:Reference number: A90198; MUID:77021516; PMID:823945
 A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
 A:Accession: A90198
 A:Molecule type: protein
 A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
 A:Note: this protein lacks most of the V region, all of the CH1 region, and part of the
 R:Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;
 Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
 A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
 A:Reference number: A93915; MUID:82247835; PMID:6808505
 A:Contents: heavy chain disease protein Om
 A:Accession: A93915
 A:Molecule type: mRNA
 A:Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157
 A:Note: a carboxyl-terminal Lys is removed posttranslationally
 A:Note: this sequence may represent an allelic form or another gamma chain subclass
 C:Comment: The heavy chain disease protein Wis is shown.
 C:Genetics:
 A:Gene: GDB:103939; OMIM:147120
 A:Cross-references: GDB:119339; OMIM:147120
 A:Map position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglytamic acid
 F:203-270/Domain: immunoglobulin homology <IMM>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 49.9%; Score 1121; DB 1; Length 289;
 Best Local Similarity 90.3%; Pred. No. 5.8e-64;
 Matches 204; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 2 DKHTCPAPALGPGSVFLPPPKPTLMISRTPEVTCVVVDVSHEDPEVKENNYVD 61
 DB 64 DTPPPCPAPALGPGSVFLPPPKPTLMISRTPEVTCVVVDVSHEDPEVQFKWYD 123
 QY 62 GVEVHNKAKTPREQNSTYRVVSVLTFLHQLDGLNGKEYKCKVSNKALPAPIETKISKAK 121
 DB 124 GVQVHNKAKTPREQNSTYRVVSVLTFLHQLDGLNGKEYKCKVSNKALPAPIETKISKAK 183
 QY 122 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLS 181
 DB 184 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLS 243
 QY 182 DGSFFLYSKLTVDKSRWQOGNPFSCSMHEALHNHYTQKSLSLSPG 227
 DB 244 DGSFFLYSKLTVDKSRWQOGNPFSCSMHEALHNHYTQKSLSLSPG 289

RESULT 10
 GHRB
 Ig gamma chain C region - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
 C:Accession: A91749; A90290; A93928; A90245; A94416; A02161
 R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
 Immunogenetics 18, 387-397, 1983
 A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haploty
 A:Reference number: A91749; MUID:84030930; PMID:61313520
 A:Accession: A91749
 A:Molecule type: mRNA
 A:Residues: 1-323 <BER>
 A:Cross-references: UNIPROT:P01870
 A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
 R:Pratt, D.M.; Mole, L.E.
 Biochem. J. 151, 337-349, 1975
 A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
 A:Reference number: A90290; MUID:76135469; PMID:1243651
 A:Accession: A90290
 A:Molecule type: protein
 A:Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>
 R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
 A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
 A:Reference number: A93928; MUID:83299917; PMID:6193512
 A:Accession: A93928
 A:Molecule type: mRNA
 A:Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
 A:Cross-references: GDB:16426; MUID:615111; PIDN:AAA31289.1; PID:G165112
 A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker;
 R:Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
 Biochem. J. 116, 249-259, 1970
 A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin
 A:Reference number: A90245; MUID:70110015; PMID:5461106
 A:Accession: A90245
 A:Molecule type: protein
 A:Residues: 132-143, 'E', 145-161 <FRU>
 R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
 In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
 A:Reference number: A94416
 A:Accession: A94416
 A:Molecule type: protein
 A:Residues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q', ;
 A:Note: this has the e15 allotypic marker, 185-Ala
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-82/Domain: immunoglobulin homology <IM1>
 F:130-199/Domain: immunoglobulin homology <IM2>
 F:236-303/Domain: immunoglobulin homology <IM3>
 F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.9%; Score 918.5; DB 1; Length 323;
 Best Local Similarity 71.7%; Pred. No. 4.2e-51;
 Matches 167; Conservative 29; Mismatches 32; Indels 5; Gaps 2;

QY 1 MDKTT---HTC--PPCPAPALGPGSVFLPPPKPTLMISRTPEVTCVVVDVSHEDPEVK 55
 DB 91 VDKTVAPSTCKPTCPPELGGPSVFIIPPKPTLMISRTPEVTCVVVDVSDDDPEVQ 150
 QY 56 FNNYDGVGVHNAKTPREQNSTYRVVSVLTFLHQLDGLNGKEYKCKVSNKALPAPIEK 115
 DB 151 FTWYINNEQVTRAPPLRQEQNSTYRVVSVLTFLHQLDGLNGKEYKCKVSNKALPAPIEK 210
 QY 116 TISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 175
 DB 211 TISKARGQPLEPKVYTMGPPRELSRSVSLTCMNGFYPSDISVEWENKGAEDNYKT 270
 QY 176 PPVLSDDGSFFLYSKLTVDKSRWQOGNPFSCSMHEALHNHYTQKSLSLSPG 228
 DB 271 PAVLSDSGSYFLYKLSVPTSEWQRGDVFSCSMHEALHNHYTQKSISRSPG 323

RESULT 11
 147160

Ig gamma 2b chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47160
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: I47158; MUID:95015845; PMID:7930579
A/Accession: I47160
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <KAC>
A/Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126
C/Genetics:
A/Gene: IgG2b
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 40.4%; Score 906.5; DB 2; Length 328;
Best Local Similarity 73.2%; Pred. No. 2.4e-50;
Matches 164; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

QY 7 CPCCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
DB 106 CPICPACE-SPGSEVFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164
QY 67 NAKTKPREQYNSTYRVSVLTPLVHODWLNKGEYKCKVSNKALPAPIETKISKAKGPQRE 126
DB 165 TAQTRPKEQFNSTYRVSVLTPLVHODWLNKGEYKCKVSNKALPAPIETKISKAKGPQRE 224
QY 127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQ--PENNYKTTTPVLDSDGS 184
DB 225 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQ--PENNYKTTTPVLDSDGS 284
QY 185 FFLYSLKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 228
DB 285 YFLYKSFVDKASWQGGIFQCAVMEALHNNHYTKSLSPGK 328

RESULT 12
I47159
Ig gamma 2a chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47159
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: I47158; MUID:95015845; PMID:7930579
A/Accession: I47159
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <KAC>
A/Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124
C/Genetics:
A/Gene: IgG2a
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 40.4%; Score 906.5; DB 2; Length 328;
Best Local Similarity 73.2%; Pred. No. 2.4e-50;
Matches 164; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

QY 7 CPCCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
DB 106 CPICPACE-SPGSEVFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164
QY 67 NAKTKPREQYNSTYRVSVLTPLVHODWLNKGEYKCKVSNKALPAPIETKISKAKGPQRE 126
DB 165 TAQTRPKEQFNSTYRVSVLTPLVHODWLNKGEYKCKVSNKALPAPIETKISKAKGPQRE 224
QY 127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQ--PENNYKTTTPVLDSDGS 184

DB 225 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQ--PENNYKTTTPVLDSDGS 284
QY 185 FFLYSLKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 228
DB 285 YFLYKSFVDKASWQGGIFQCAVMEALHNNHYTKSLSPGK 328

RESULT 13
I47162
Ig gamma 4 chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47162
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: I47158; MUID:95015845; PMID:7930579
A/Accession: I47162
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-277 <KAC>
A/Cross-references: EMBL:U03782; NID:G433129; PIDN:AAA52220.1; PID:G433130
C/Genetics:
A/Gene: IgG4
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 40.2%; Score 903.5; DB 2; Length 277;
Best Local Similarity 71.1%; Pred. No. 3.1e-50;
Matches 167; Conservative 30; Mismatches 31; Indels 7; Gaps 4;

QY 1 MDK---THTCPPCP-APELLG-GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55
DB 43 VDKRVGVTGTPCPCIPACGPGPSAFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 102
QY 56 FNNYVDGVEVHNAKTPREQYNSTYRVSVLTPLVHODWLNKGEYKCKVSNKALPAPIETK 115
DB 103 FSWYVDGVEVHTAQRPEQFNSTYRVSVLTPLVHODWLNKGEYKCKVSNKALPAPIETK 162
QY 116 TISKAGQPREQYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQ--PENNYK 173
DB 163 IISKAGQPREQYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQ--PENNYK 222
QY 174 TTPPVLSDSGSFFLYSLKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 228
DB 223 TTPPQDQDVGTYFLYSLKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 277

RESULT 14
GZGP
Ig gamma-2 chain C region - guinea pig
C/Species: Cavia porcellus (guinea pig)
C/Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C/Accession: A94553; A90352; A90359; A90384; A90385; A02151
R/Trischmann, T.M.
submitted to the Atlas, April 1975
A/Reference number: A94553
A/Accession: A94553
A/Molecule type: protein
A/Residues: 1-3 <TRI>
A/Cross-references: UNIPROT:P01862
R/Birshstein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A/Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
A/Reference number: A90352; MUID:71058471; PMID:538606
A/Accession: A90352
A/Molecule type: protein
A/Residues: 4-68 <BIN>
R/Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A/Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am
A/Reference number: A90359; MUID:71058486; PMID:538616
A/Accession: A90359

A:Molecule type: protein
A:Residues: 69-133,312-329 <TR>
R:Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90384; MUID:75036072; PMID:4429665
A:Accession: A90384
A:Molecule type: protein
A:Residues: 134-226 <TRA>
R:Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90385; MUID:75036073; PMID:4609467
A:Accession: A90385
A:Molecule type: protein
A:Residues: 227-311 <TR2>
R:Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A:Reference number: A90354; MUID:71058474; PMID:4922544
A:Contents: annotation; disulfide bonds
A:Note: Cys-16 is involved in a heavy-light chain bond
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:21-81/Domain: immunoglobulin homology <IM1>
F:135-204/Domain: immunoglobulin homology <IM2>
F:241-310/Domain: immunoglobulin homology <IM3>
F:28-79/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Asn) (covalent)
F:248-308/Disulfide bonds: #status experimental

Query Match 39.6%; Score 889; DB 1; Length 329;
Best Local Similarity 72.3%; Pred. No. 3.1e-49;
Matches 162; Conservative 24; Mismatches 36; Indels 2; Gaps 1;
6 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDQVEV 65
106 TCPCPPENLGGPSVFIAPPKPKDTLMISLTPRVTCTVVVDVSDQDEPEVQFTWVDNKPV 165
66 HNAKTPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
166 GNAETKPRVEQNTTFRVESVLPVQHODWLGKGEKCKVYKALPAPIEKTISKTKDAPR 225
126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVLDSDG 183
226 MPDVYTLPPSRDELTKSKSVTCLIIINFPFADIHVEWASNRVFSVEKEYKNTPTIEDADG 285
184 SPFLYSKLTVDKSRWQQGVNFSCSVNHEALHNHYTQKSLSLSPG 227
286 SYFLYSKLTVDKSAWDQGVITTCVSNVHEALHNHYTQKLSRSPG 329

RESULT 15
I47158
Ig gamma 1 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47158
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47158
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03778; NID:g4333121; PIDN:AAA52216.1; PID:g4333122
C:Genetics:

A:Gene: IgG1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IM>

Query Match 39.4%; Score 885.5; DB 2; Length 328;
Best Local Similarity 72.4%; Pred. No. 5.2e-49;
Matches 163; Conservative 27; Mismatches 32; Indels 3; Gaps 2;
6 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDQVEV 65
105 TCPCPCGCE-VAGPSVFIPPPKPKDTLMISQTPETCVVVDVSKHAEVQFSWYVDGVEV 163
66 HNAKTPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
164 HTAETRPKEEQNFNYSVSVLPVQHODWLGKGEKCKVNNVDLPAPITRTISKALGQSR 223
126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--PENNYKTTTPPVLDSDG 183
224 EPQVYTLPPPAEELSRSKVTCLVIGFYPPIHVEWKSNGQPEPENTYRTTTPPQDDVDG 283
184 SPFLYSKLTVDKSRWQQGVNFSCSVNHEALHNHYTQKSLSLSPGK 228
284 TFFLYSKLAVDKARWDHGDGKPECAVWHEALHNHYTQKSISTQGGK 328

Search completed: March 8, 2005, 14:46:15
Job time : 16.3429 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:56 ; Search time 74.1412 Seconds
(without alignments)
2769.633 Million cell updates/sec

Title: US-09-389-782A-8
Perfect score: 2246
Sequence: 1 MKTHTCPCPAPPELLGGPS.....QKGNATHDNCISNSESSTOK 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1233	54.9	330	1	GCL_HUMAN	P01857 homo sapien
2	1233	54.9	465	2	Q6GMX6	Q6gmxx6 homo sapien
3	1233	54.9	466	2	Q6IN78	Q6in78 homo sapien
4	1233	54.9	469	2	Q7Z7P5	Q7z7p5 homo sapien
5	1233	54.9	470	2	Q6PJA4	Q6pj44 homo sapien
6	1233	54.9	470	2	Q7Z5W1	Q7z5w1 homo sapien
7	1233	54.9	472	2	Q6N089	Q6n089 homo sapien
8	1233	54.9	475	2	Q6GMW7	Q6gmw7 homo sapien
9	1233	54.9	476	2	Q6GMX1	Q6gmxx1 homo sapien
10	1233	54.9	679	2	Q96PQ8	Q96pq8 homo sapien
11	1229	54.7	473	2	Q6P055	Q6p055 homo sapien
12	1229	54.7	475	2	Q6MZQ6	Q6mzq6 homo sapien
13	1229	54.7	480	2	Q6N094	Q6n094 homo sapien
14	1229	54.7	481	2	Q6N097	Q6n097 homo sapien
15	1229	54.7	482	2	Q7Z351	Q7z351 homo sapien
16	1227	54.6	348	2	Q6PYX1	Q6pyx1 homo sapien
17	1227	54.6	473	2	Q6MZV7	Q6mzv7 homo sapien
18	1227	54.6	478	2	Q6P181	Q6p181 homo sapien
19	1227	54.6	480	2	Q6P1F1	Q6p1f1 homo sapien
20	1226	54.6	466	2	Q6N096	Q6n096 homo sapien
21	1222	54.4	475	2	Q6N095	Q6n095 homo sapien
22	1222	54.4	544	2	Q6PJ95	Q6pj95 homo sapien
23	1216	54.1	487	2	Q652L2	Q652l2 mus sp. fv/
24	1146	51.0	354	2	Q86T22	Q86tt2 homo sapien
25	1146	51.0	518	2	Q6N030	Q6n030 homo sapien
26	1142.5	50.9	326	1	GCL_HUMAN	P01859 homo sapien
27	1142.5	50.9	417	2	Q6N093	Q6n093 homo sapien
28	1142	50.8	521	2	Q8N4V9	Q8n4v9 homo sapien
29	1139.5	50.7	464	2	Q6MZU6	Q6mzu6 homo sapien
30	1137.5	50.6	465	2	Q6P6C4	Q6p6c4 homo sapien
31	1135	50.5	327	1	GCL_HUMAN	P01861 homo sapien

32	1135	50.5	473	2	Q8TC63	Q8tc63 homo sapien
33	1131	50.4	509	2	Q8NF17	Q8nf17 homo sapien
34	1128.5	50.2	493	2	Q68CN4	Q68cn4 homo sapien
35	1126	50.1	290	1	GC3_HUMAN	P01860 homo sapien
36	1126	50.1	476	2	Q6MZX7	Q6mzx7 homo sapien
37	1009	44.9	401	1	T11B_HUMAN	O00300 homo sapien
38	918.5	40.9	323	1	GC_RABIT	P01870 oryctolagus
39	909	40.5	337	2	Q95W34	Q95w34 equus caball
40	892	39.7	401	2	Q6P112	Q6p112 mus musculus
41	889	39.6	329	1	GC2_CAVPO	P01862 cavia porce
42	888	39.5	401	1	T11B_MOUSE	O08712 mus musculus
43	875	39.0	401	1	T11B_RAT	O08727 rattus norv
44	845.5	37.6	329	1	GC3_MOUSE	P22436 mus musculus
45	845.5	37.6	470	2	Q7TNK1	Q7tnk1 mus musculus

ALIGNMENTS

RESULT 1
GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;


```

Qy 62 GVEVHNKTPREEQNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIKTIKAK 121
Db 164 GVEVHNKTPREEQNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIKTIKAK 223
Qy 122 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
Db 224 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 283
Qy 182 DGSFFLYSKLTVDKSRWQOQNVFSCSVMEALHNNHYTKSLSLSPGK 228
Db 284 DGSFFLYSKLTVDKSRWQOQNVFSCSVMEALHNNHYTKSLSLSPGK 330

RESULT 2
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

```

Query Match 54.9%; Score 1233; DB 2; Length 465;
 Best Local Similarity 100.0%; Pred. No. 6.8e-73;

```

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DKHTHTCCPAPBELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 239 DKHTHTCCPAPBELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 298
Qy 62 GVEVHNKTPREEQNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIKTIKAK 121
Db 299 GVEVHNKTPREEQNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIKTIKAK 358
Qy 122 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
Db 359 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 418
Qy 182 DGSFFLYSKLTVDKSRWQOQNVFSCSVMEALHNNHYTKSLSLSPGK 228
Db 419 DGSFFLYSKLTVDKSRWQOQNVFSCSVMEALHNNHYTKSLSLSPGK 465

RESULT 3
Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.

```



```

DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCBDB81076E CRC64;

Query Match
Best Local Similarity 54.9%; Score 1233; DB 2; Length 466;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCTCPAPALGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 240 DKHTCTCPAPALGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 299
QY 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 121
DB 300 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 359
QY 122 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
DB 360 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 419
QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 228
DB 420 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 466

RESULT 4
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Malek J.A., Gunaratne P.H.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.

```

```

DR PROSITE; PS00835; IG_LIKE; 4.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match
Best Local Similarity 54.9%; Score 1233; DB 2; Length 469;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCTCPAPALGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 243 DKHTCTCPAPALGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 302
QY 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 121
DB 303 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 362
QY 122 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
DB 363 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 422
QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 228
DB 423 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 469

RESULT 5
Q6PJ44 PRELIMINARY; PRT; 470 AA.
AC Q6PJ44
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.

```

```
DR Pfam: PF07654; Cl-set; 3.
DR SMART: SM00409; IG 2.
DR SMART: SM00407; IGcl; 3.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
DR KW Hypothetical protein_2.
DR KW Hypothetical protein_2.
SQ SEQUENCE 470 AA; 51715 MW; 7849556A11FD7D99 CRC64;

Query Match 54.9%; Score 1233; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 6.9e-73;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCTCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 244 DKHTCTCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 303
QY 62 GVEVHNKATKPREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIETISKAK 121
DB 304 GVEVHNKATKPREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIETISKAK 363
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
DB 364 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 423
QY 182 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 228
DB 424 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 470

RESULT 6
Q7Z5W1 PRELIMINARY; PRT; 470 AA.
AC Q7Z5W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vialalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC053984; AAH53984.1; -.
DR HSSP: P01857; 1HZH.

Query Match 54.9%; Score 1233; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 6.9e-73;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCTCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 244 DKHTCTCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 303
QY 62 GVEVHNKATKPREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIETISKAK 121
DB 304 GVEVHNKATKPREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIETISKAK 363
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
DB 364 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 423
QY 182 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 228
DB 424 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 470

RESULT 7
Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX640627; CAE45781.1; -.
DR HSSP: P01861; 1ADQ.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF07654; Cl-set; 3.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGcl; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
DR KW Hypothetical protein.
DR KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 54.9%; Score 1233; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 6.9e-73;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCTCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
```

```

Db 246 DKTHCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 305
Qy 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 306 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 365
Qy 122 GQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
Db 366 GQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 425
Qy 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
Db 426 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 472

RESULT 8
Q6GMW7 PRELIMINARY; PRT; 475 AA.
AC Q6GMW7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ Hypothetical protein.
SEQUENCE 475 AA; 51987 MW; 2A1P55D736860F8 CRC64;

```

```

Query Match 54.9%; Score 1233; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 6.9e-73;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DKTHCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 249 DKTHCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 308
Qy 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 309 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 368
Qy 122 GQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
Db 369 GQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 428
Qy 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
Db 429 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 475

RESULT 9
Q6GMX1 PRELIMINARY; PRT; 476 AA.
ID Q6GMX1
AC Q6GMX1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IGC1; 3.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.

```

DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 476 AA; 52286 MW; 622AABAS62DD89D CRC64;
 Query Match 54.9%; Score 1233; DB 2; Length 476;
 Best Local Similarity 100.0%; Pred. No. 7e-73;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DKHTCCPPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
 DB 250 DKHTCCPPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 309
 QY 62 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
 DB 310 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 369
 QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDS 181
 DB 370 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDS 429
 QY 182 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
 DB 430 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
 RESULT 10
 Q96PQ8 PRELIMINARY; PRT; 679 AA.
 AC Q96PQ8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Factor VII active site mutant immunoconjugate.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
 RA Hu Z., Garen A.;
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
 cells for immunotherapy in mouse models of prostatic cancer."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu Z., Garen A.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF272774; AAK58686.2; -;
 DR HSSP; P08709; 1KLI.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004235; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPRO00152; Asx hydroxyl_s.
 DR InterPro; IPRO001742; EGF_2.
 DR InterPro; IPRO01881; EGF_Ca.
 DR InterPro; IPRO06209; EGF_Like.
 DR InterPro; IPRO07110; Ig-like.
 DR InterPro; IPRO03597; Ig_c1.
 DR InterPro; IPRO03006; Ig_MHC.
 DR InterPro; IPRO01254; Peptidase s1.
 DR InterPro; IPRO09003; Pept Ser Cys.
 DR InterPro; IPRO00294; VitK_dep_GLA.
 DR Pfam; PF07654; Cl-set; 2.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA_1.
 DR SMART; SM00407; IGC1; 1.

DR SMART; SM00020; TYD_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;
 Query Match 54.9%; Score 1233; DB 2; Length 679;
 Best Local Similarity 100.0%; Pred. No. 1e-72;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DKHTCCPPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
 DB 453 DKHTCCPPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 512
 QY 62 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
 DB 513 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 572
 QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDS 181
 DB 573 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDS 632
 QY 182 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
 DB 633 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 679
 RESULT 11
 Q6P055 PRELIMINARY; PRT; 473 AA.
 ID Q6P055;
 AC Q6P055;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield J.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

```

RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strauberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -.
DR HSSP; P01861; 1ADQ
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 54.7%; Score 1229; DB 2; Length 473;
Best Local Similarity 99.6%; Pred. No. 1.3e-72;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 247 DKHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 306
QY 62 GVEVHNAKTPREEQNSTYRVVSVLTVLHODWLNKKEYKCKVSNKALPAPIETKISKAK 121
DB 307 GVEVHNAKTPREEQNSTYRVVSVLTVLHODWLNKKEYKCKVSNKALPAPIETKISKAK 366
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
DB 367 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 426
QY 182 DGSFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTKQSLSLSPGK 228
DB 427 DGSFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTKQSLSLSPGK 473

RESULT 12
Q6MZQ6 PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G1190.
GN Name=DKFZp686G1190;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 480 AA; 52612 MW; 225247FD3D35ABC18 CRC64;

Query Match 54.7%; Score 1229; DB 2; Length 480;
Best Local Similarity 99.6%; Pred. No. 1.3e-72;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 254 DKHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 313
QY 62 GVEVHNAKTPREEQNSTYRVVSVLTVLHODWLNKKEYKCKVSNKALPAPIETKISKAK 121
DB 314 GVEVHNAKTPREEQNSTYRVVSVLTVLHODWLNKKEYKCKVSNKALPAPIETKISKAK 373

us-09-389-782a-8.rup

```

```
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
DB 374 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 433
QY 182 DGSFFLYSKLTVDKSRWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 228
DB 434 DGSFFLYSKLTVDKSRWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 480

RESULT 14
ID Q6N097 PRELIMINARY; PRT; 481 AA.
AC Q6N097;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFp686H20196.
GN Name=DKFp686H20196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP TISSUE=Human rectum tumor;
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640619; CAB45773.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52759 MW; 47220D9B64BDF98B CRC64;

Query Match 54.7%; Score 1229; DB 2; Length 481;
Best Local Similarity 99.6%; Pred. No. 1.3e-72;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKHTCCPCPAPPELLGGPSVFLPPLPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 255 DKHTCCPCPAPPELLGGPSVFLPPLPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 314
QY 62 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 315 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 374
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
DB 375 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 434
QY 182 DGSFFLYSKLTVDKSRWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 228
DB 435 DGSFFLYSKLTVDKSRWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 481

RESULT 15
ID Q7Z351 PRELIMINARY; PRT; 482 AA.
AC Q7Z351;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
DE Hypothetical protein DKFp686N02209.
GN Name=DKFp686N02209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP TISSUE=Human rectum tumor;
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538118; CAD98026.1; -.
DR HSSP; P01857; IHZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;

Query Match 54.7%; Score 1229; DB 2; Length 482;
Best Local Similarity 99.6%; Pred. No. 1.3e-72;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKHTCCPCPAPPELLGGPSVFLPPLPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 256 DKHTCCPCPAPPELLGGPSVFLPPLPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 315
QY 62 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 316 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 375
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
DB 376 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 435
QY 182 DGSFFLYSKLTVDKSRWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 228
DB 436 DGSFFLYSKLTVDKSRWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 482

Search completed: March 8, 2005, 14:44:40
Job time : 74.1412 secs
```

This Page Blank (uspto)